

APPENDIX

Error! Unknown document property name.



Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Bio

Search for

Show:

☐ 1: NP_599320. two-component sys...[gi:19551318] BLink, Domains, Links

LOCUS NP_599320 551 aa linear BCT 12-JAN-2004

DEFINITION two-component system sensory transduction histidine kinase
[Corynebacterium glutamicum ATCC 13032].

ACCESSION NP_599320

VERSION NP_599320.1 GI:19551318

DBSOURCE REFSEQ: accession NC_003450.2

KEYWORDS

SOURCE Corynebacterium glutamicum ATCC 13032

ORGANISM Corynebacterium glutamicum ATCC 13032

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE 1

AUTHORS Nakagawa, S.

TITLE Complete genomic sequence of Corynebacterium glutamicum ATCC 13032

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 551)

AUTHORS NCBI Genomes Project.

TITLE Direct Submission

JOURNAL Submitted (23-SEP-2002) National Center for Biotechnology

Information, NIH, Bethesda, MD 20894, USA

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
reference sequence was derived from NCg10067.

Genome re-annotation resulted from the combination of the
Corynebacterium glutamicum complete genomes deposited in GenBank
Accession Numbers BA000036 and NC_003450. The first version of
NC_003450 was derived from AX000000. BA000036 has a single 'c'
insertion at position 2231350 compared to AX000000. First version
of NC_003450 was annotated by NCBI staff using the GenMark HMM
prediction program and BLAST analysis results. Cgl#### systematic
gene names were used but the same gene names were later re-used in
BA000036 record. To avoid the confusion in the the present record
NCg1#### refers to the new systematic gene name for the revised
version of the Corynebacterium glutamicum genome, whereas, Cgl###
refers to the corresponding gene in the Corynebacterium glutamicum
complete genome deposited at GenBank Accession Number BA000036.
Method: conceptual translation.

FEATURES

source

Location/Qualifiers

1..551

/organism="Corynebacterium glutamicum ATCC 13032"

/db_xref="taxon:196627"

Protein

1..551

/product="two-component system sensory transduction
histidine kinase"

/EC_number="2.7.3.-"

CDS

1..551

/locus_tag="NCg10067"

/coded_by="NC_003450.2:70506..72161"

/note="similar to signal transduction histidine kinase
regulating citrate/malate metabolism"

/transl_table=11
/db_xref="GeneID:1021092"

ORIGIN

1 msvgggsdwkn fkevdiiirfa trilviqvav valvvaictg ifavlmmndqm ktqaehtals
61 igrsvasnpq ireevaldtq tganpsaeel adgdiqavaq aanertgalf vvitdglgir
121 lshpdeerlg eqvstsfeaa mrgeetmawe tgtlgasara kvpifapdss vpvgevsvgf
181 erdsvysrlp mflaalalis vlgiligvgv amgmrrrwer vtlglqpeel vtlvqnqtav
241 idgidegvla lspngtigvh neqaqsmiga gpmsgrtlke lgldlgldgv vlhgqhpetv
301 ahngrilyld fhpvrregdq lgyvvtirdr tdielserl dsvrtmthal raqrhefanr
361 ihtatglida grvhdaaefl gdisrnggqs hpligsahln eafllssflst asisasekgv
421 slrinsdtli lgtvkdpedv atilgnlinn aidaavagea prwieltlmd dadtlvisva
481 dsgpgipegv dvfatatqig dsednerthg hgigklcra larshggdvw vidrgtedga
541 vfgvklpgvm e

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Jan 12 2004 10:46:34



results of BLAST

BLASTP 2.2.7 [Jan-02-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1074192799-32432-13245777434.BLASTQ4

Query=

(551 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

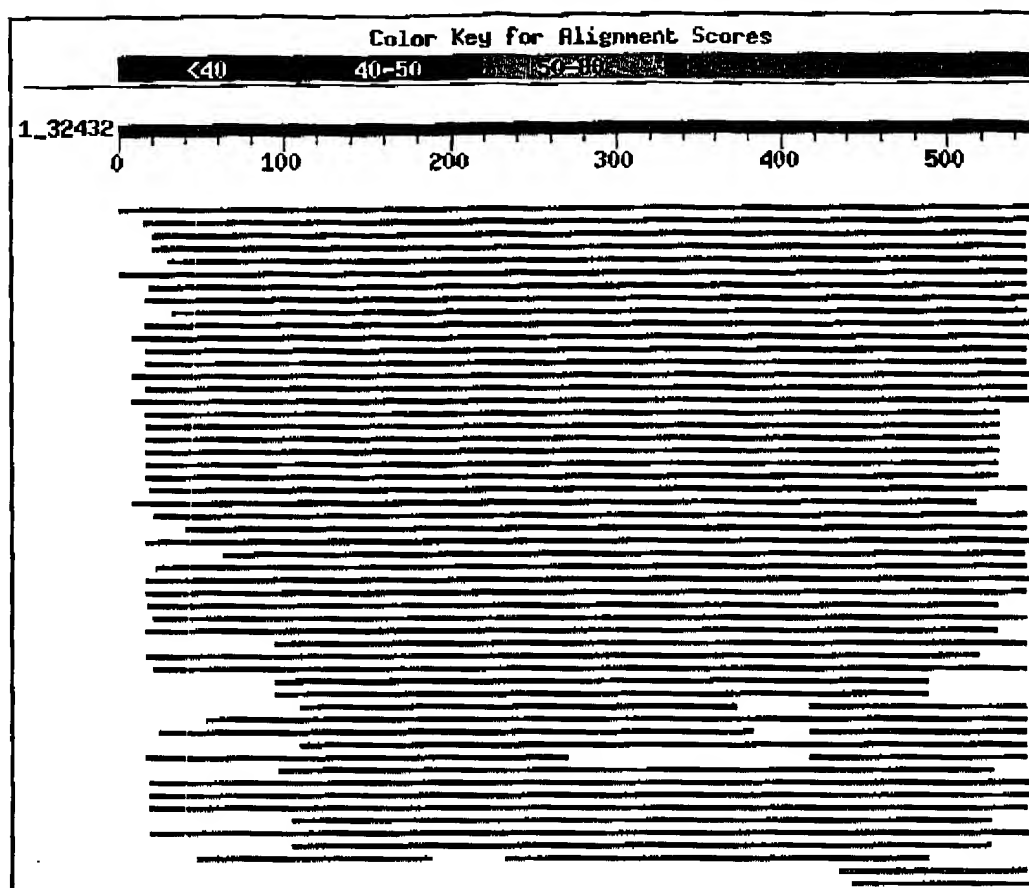
1,605,642 sequences; 528,039,549 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:

Score E
(bits) Value

gi 19551318 ref NP_599320.1	two-component system sensory t...	983	0.0
gi 25029461 ref NP_739515.1	putative sensor kinase [Coryne...	594	e-168
gi 21224173 ref NP_629952.1	putative two-component sensor ...	214	4e-54
gi 29828972 ref NP_823606.1	putative two-component system ...	213	1e-53
gi 15616401 ref NP_244706.1	two-component sensor histidine...	172	1e-41
gi 15640810 ref NP_230440.1	sensor kinase cita [Vibrio cho...	167	4e-40
gi 29829358 ref NP_823992.1	putative two-component system ...	162	2e-38
gi 21398877 ref NP_654862.1	HATPase_c, Histidine kinase-, ...	160	7e-38
gi 16080204 ref NP_391030.1	similar to two-component senso...	159	1e-37
gi 30019091 ref NP_830722.1	Two-component sensor kinase ci...	158	2e-37
gi 15800334 ref NP_286346.1	putative sensor-type protein [...	156	9e-37
gi 30260717 ref NP_843094.1	sensor histidine kinase [Bacil...	155	2e-36
gi 16767554 ref NP_463169.1	sensory histidine kinase [Salm...	154	4e-36
gi 16128602 ref NP_415152.1	putative sensor-type protein [...	153	7e-36
gi 16762986 ref NP_458603.1	two-component sensor kinase [S...	153	7e-36
gi 26246600 ref NP_752639.1	Sensor kinase dpiB [Escherichi...	153	9e-36
gi 15804717 ref NP_290758.1	putative 2-component sensor pr...	152	2e-35
gi 536970 gb AAA97025.1 ORF	f543 [Escherichia coli]	152	2e-35
gi 24115306 ref NP_709816.1	putative 2-component sensor pr...	152	2e-35
gi 27365978 ref NP_761506.1	signal transduction histidine ...	151	4e-35
gi 26250939 ref NP_756979.1	Sensor protein dcuS [Escherich...	151	4e-35

gi 37679787 ref NP 934396.1	putative sensor kinase Cita [V...	150	5e-35
gi 21223794 ref NP 629573.1	putative two-component sensor ...	149	1e-34
gi 2734636 gb AAC28951.1	histidine kinase [Escherichia coli]	148	2e-34
gi 15612960 ref NP 241263.1	two-component sensor histidine...	147	4e-34
gi 30018746 ref NP 830377.1	Two component system histidine...	147	7e-34
gi 16764002 ref NP 459617.1	sensory histidine kinase [Salm...	145	2e-33
gi 21219651 ref NP 625430.1	putative two component system ...	145	2e-33
gi 23100706 ref NP 694173.1	two-component sensor histidine...	144	5e-33
gi 16759585 ref NP 455202.1	sensor kinase DpiB [Salmonella...	144	5e-33
gi 28898486 ref NP 798091.1	putative sensor kinase Cita [V...	141	4e-32
gi 28211194 ref NP 782138.1	sensor kinase dpiB [Clostridiu...	140	8e-32
gi 23100675 ref NP 694142.1	two-component sensor histidine...	136	9e-31
gi 15641613 ref NP 231245.1	sensor kinase cita, putative [...	131	4e-29
gi 23112843 ref ZP 00098276.1	COG3290: Signal transduction...	131	4e-29
gi 18309513 ref NP 561447.1	two-component sensor histidine...	130	9e-29
gi 16077825 ref NP 388639.1	two-component sensor histidine...	128	3e-28
gi 21398531 ref NP 654516.1	HATPase_c, Histidine kinase-li...	127	8e-28
gi 30018763 ref NP 830394.1	Two-component sensor kinase yu...	125	2e-27
gi 23007702 ref ZP 00049454.1	COG3290: Signal transduction...	124	6e-27
gi 16077512 ref NP 388326.1	similar to two-component senso...	117	6e-25
gi 29375782 ref NP 814936.1	sensory box histidine kinase [...	116	9e-25
gi 15615315 ref NP 243618.1	two-component sensor histidine...	115	2e-24
gi 21398509 ref NP 654494.1	hypothetical protein predicted...	110	6e-23
gi 28900618 ref NP 800273.1	putative sensor kinase Cita [V...	110	7e-23
gi 29140597 ref NP 803939.1	sensor kinase Cita [Salmonella...	107	5e-22
gi 16759047 ref NP 454664.1	sensor kinase cita [Salmonella...	107	6e-22
gi 1705888 sp P52687 CITA KLEPN	Sensor kinase cita >gi 2126...	106	1e-21
gi 27366560 ref NP 762087.1	Signal transduction histidine ...	104	4e-21
gi 16763443 ref NP 459058.1	putative transcriptional regul...	103	1e-20
gi 37676272 ref NP 936668.1	putative sensor kinase Cita [V...	97	8e-19
gi 21219206 ref NP 624985.1	putative integral membrane sen...	94	6e-18
gi 21910305 ref NP 664573.1	putative two-component sensor ...	93	1e-17
gi 15675090 ref NP 269264.1	putative two-component sensor ...	92	3e-17
gi 19746058 ref NP 607194.1	putative two-component sensor ...	91	5e-17
gi 23121699 ref ZP 00103912.1	COG3290: Signal transduction...	89	2e-16
gi 22538059 ref NP 688910.1	sensor histidine kinase [Strep...	87	1e-15
gi 25011947 ref NP 736342.1	Unknown [Streptococcus agalact...	87	1e-15
gi 28894462 gb AAO61209.1	putative integral membrane senso...	85	3e-15
gi 29827327 ref NP 921961.1	putative membrane protein [Str...	80	8e-14
gi 29830694 ref NP 825328.1	hypothetical protein [Streptom...	72	3e-11
gi 37521385 ref NP 924762.1	two-component sensor histidine...	70	2e-10
gi 34810596 pdb 1OJG A	Chain A, Sensory Domain Of The Membr...	65	4e-09
gi 22968402 ref ZP 00015990.1	COG2200: FOG: EAL domain [Rh...	64	1e-08
gi 33240571 ref NP 875513.1	Signal transduction histidine ...	63	2e-08
gi 16127201 ref NP 421765.1	sensory box histidine kinase/r...	62	3e-08
gi 17229920 ref NP 486468.1	two-component hybrid sensor an...	62	4e-08
gi 18450332 ref NP 569203.1	pli0050 [Listeria innocua] >gi...	61	6e-08
gi 22962960 ref ZP 00010566.1	COG0642: Signal transduction...	59	2e-07
gi 23040362 ref ZP 00071878.1	COG0642: Signal transduction...	59	2e-07
gi 39934055 ref NP 946331.1	sensor histidine kinase with a...	59	3e-07
gi 22987306 ref ZP 00032387.1	COG0784: FOG: CheY-like rece...	59	3e-07
gi 23125546 ref ZP 00107475.1	COG0784: FOG: CheY-like rece...	59	3e-07
gi 17231092 ref NP 487640.1	two-component sensor histidine...	59	3e-07
gi 33865287 ref NP 896846.1	two-component sensor histidine...	59	3e-07
gi 11362593 pir T50637	probable histidine kinase [imported...	59	3e-07
gi 20092217 ref NP 618292.1	sensory transduction histidine...	58	4e-07
gi 17548102 ref NP 521504.1	PROBABLE TWO-COMPONENT SENSOR ...	58	6e-07
gi 23473200 ref ZP 00128496.1	COG0642: Signal transduction...	57	7e-07
gi 28869841 ref NP 792460.1	bacteriophytochrome, putative ...	57	7e-07
gi 11497642 ref NP 068862.1	signal-transducing histidine k...	57	8e-07

gi 37523781	ref NP_927158.1	two-component hybrid sensor an...	57	1e-06
gi 18310298	ref NP_562232.1	two-component sensor histidine...	57	1e-06
gi 23471590	ref ZP_00126919.1	COG4251: Bacteriophytochrome...	56	1e-06
gi 38232698	ref NP_938465.1	Putative two-component system ...	56	1e-06
gi 22651420	gb AAL13332.1	bZIP histidine kinase [Pseudomon...	51	6e-05
gi 23109029	ref ZP_00095226.1	COG2202: FOG: PAS/PAC domain...	56	1e-06
gi 16125186	ref NP_419750.1	sensor histidine kinase/respon...	56	1e-06
gi 29829895	ref NP_824529.1	putative two-component system ...	56	1e-06
gi 23026365	ref ZP_00064851.1	COG2202: FOG: PAS/PAC domain...	56	2e-06
gi 15672378	ref NP_266552.1	sensor protein kinase [Lactoco...	56	2e-06
gi 37519945	ref NP_923322.1	two-component sensor histidine...	56	2e-06
gi 28199553	ref NP_779867.1	two-component system, sensor p...	56	2e-06
gi 23012921	ref ZP_00052899.1	COG0642: Signal transduction...	56	2e-06
gi 23127740	ref ZP_00109603.1	COG0642: Signal transduction...	56	2e-06
gi 25026835	ref NP_736889.1	putative sensor kinase [Coryne...	56	2e-06
gi 22995518	ref ZP_00039994.1	COG0642: Signal transduction...	56	2e-06
gi 23055901	ref ZP_00081977.1	COG0642: Signal transduction...	56	2e-06
gi 15836992	ref NP_297680.1	two-component system, sensor p...	56	2e-06
gi 22995932	ref ZP_00040213.1	COG0642: Signal transduction...	56	2e-06

Alignments

>gi|19551318|ref|NP_599320.1| two-component system sensory transduction histidine
[Corynebacterium glutamicum ATCC 13032]
gi|21322832|dbj|BAB97461.1| Two-component system, sensory transduction histidine
[Corynebacterium glutamicum ATCC 13032]
Length = 551

Score = 983 bits (2542), Expect = 0.0

Identities = 524/551 (95%), Positives = 524/551 (95%)

Query: 1 MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMDQMKTAEHTALS 60
MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMDQMKTAEHTALS
Sbjct: 1 MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMDQMKTAEHTALS 60

Query: 61 IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIR 120
IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIR
Sbjct: 61 IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIR 120

Query: 121 LSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGF 180
LSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGF
Sbjct: 121 LSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGF 180

Query: 181 ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAV 240
ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAV
Sbjct: 181 ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAV 240

Query: 241 IDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXHGQHPETV 300
IDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKE HGQHPETV
Sbjct: 241 IDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKELGLDLGLDGVVLHGQHPETV 300

Query: 301 AHNGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANR 360
AHNGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANR
Sbjct: 301 AHNGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANR 360

Query: 361 IHTATGLIDAGRVHDAEFLGDISRNGGQSHPLIGSAHLNXXXXXXXXXXXXXKGV 420
IHTATGLIDAGRVHDAEFLGDISRNGGQSHPLIGSAHLNE BKGV
Sbjct: 361 IHTATGLIDAGRVHDAEFLGDISRNGGQSHPLIGSAHLNEAFLSSFLSTASISASEKGV 420

Query: 421 SLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVA 480
SLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVA
Sbjct: 421 SLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVA 480

Query: 481 DSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEDEGA 540
DSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEDEGA
Sbjct: 481 DSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEDEGA 540

Query: 541 VFGVKLPGVME 551
VFGVKLPGVME
Sbjct: 541 VFGVKLPGVME 551

>gi|25029461|ref|NP_739515.1| putative sensor kinase [Corynebacterium efficiens YS-
gi|23494750|dbj|BAC19715.1| putative sensor kinase [Corynebacterium efficiens YS-
Length = 556

Score = 594 bits (1532), Expect = e-168
Identities = 332/538 (61%), Positives = 406/538 (75%), Gaps = 5/538 (0%)

Query: 16 IIRFATRILVIQVATVALVVAICTGIFAVLMDQMKTEAHTALSIGRSVASNPQIREEV 75
I+RFATRILVIQV TVA+VVA+C+ +F L ++Q+K EAE +ALSI R VA++PQ+R+EV
Sbjct: 3 IMRFATRILVIQVLTVAVVAVCSAVFTFLTVEQLKAEAEQSALSISRVAADPQVRDEV 62

Query: 76 ALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVST 135
A DT TGA P+A ELA G +Q A +A TGALF+VITDG GIRL+HPD++RLG+ VST
Sbjct: 63 ARDTFTGAEPATAELARGPLQEFHAQAQVSTGALFIVITDGNGIRLAHPDQQRLLGQVVST 122

Query: 136 SFEAAMRGEETMAWETGTLGASARAKVPFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
F+AA+RGEET+AWETGTLG SARAKVP+FAP ++ PVG VSVGFER SV+ RLP L
Sbjct: 123 GFDAALRGEETIAWETGTLGESARAKVPVFAPGTTTPVGGVSVGFERASVFDRLPPLMT 182

Query: 196 LALISVLGILIGVGVAMGMRRRNRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+A +VL +++G GVA+ MRRRWE +TLGLQPEELV L++N TAV++G++EGVLAL P+G
Sbjct: 183 VAACAVLALILGAGVAVVMRRRWEITLGLQPEELVELLKNHTAVLNGVEEGVLALRPDG 242

Query: 256 TIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVR 315
TI VHN+QA+ + G ++GRTL E G P V+ N RILYLD HPV
Sbjct: 243 TIDVHNQQAIREITGIEALAGRTLPELGMDEGIVDKLLRGDRPGAVSLNNRILYLDHHPVT 302

Query: 316 RGDQDLGVVVTIADRTDIIELSERLDSVRTMTALRAQRHEFANRIHTATGLIDAGRVDH 375
RGDQ+LG+V+TIRDRTD++EL+ERLDSVRTMT ALRAQRHEF+NRIHTATGLIDAGR HD
Sbjct: 303 RGDQELGHVITIRDRTDMVELTERLDSVRTMTQALRAQRHEFSNRIHTATGLIDAGRPHD 362

Query: 376 AAFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLILGTVK 435
AA FL I +GGQ HPL+G+ L E E+GV LRI DTLILG V
Sbjct: 363 AAFLRSIGGHGGQVHPLLGAEELLEAFSSFITTAITASERGVGLRITDDTLILGEVD 422

Query: 436 DPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFAT 495
+ ED+AT+LGNL+ NAIDAA G+ PR ++LTL+DD DTLV++VAD+GPGI VDVFA
Sbjct: 423 NAEDIATVLGNLLTNAIDAAARGDEPRVDLTLLDDGDTLVMTVADTGPGITGDVDVFAA 482

Query: 496 ATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTE--DGAVFGVKLPGVME 550
+ D D HGHG+GLKL RALARS GGDVW+IDRG + GAVEG LPGVM
Sbjct: 483 PPVDDWTD--AIHGHGLGLKLRLARSLGCDVWIIDRGQPGSGAVFGASLPGVM 538

>gi|21224173|ref|NP_629952.1| putative two-component sensor [Streptomyces coelicolor
gi|7481675|pir|T35203 probable two-component sensor - Streptomyces coelicolor
gi|3036894|emb|CAA18527.1| putative two-component sensor [Streptomyces coelicolor
Length = 566

Score = 214 bits (545), Expect = 4e-54
Identities = 180/538 (33%), Positives = 269/538 (50%), Gaps = 37/538 (6%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMDQMKEAHTALSIGRSVASNPQIREEVALDTQ 80
+++L++Q+A A V + TG+F + DQ+ +A AL+I ++ A PQ+ ++
Sbjct: 30 SQVLLMQLAIAAGVAVLATGLFLAPLGDQLDDQAMRRALAIQAQTTAQPPQVVRDLRTTRP 89

Query: 81 TGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEEA 140
T A+G +Q A+ E T A +VV+ D G+R SH D ER+GE VST A
Sbjct: 90 T-----ANGFVQREAEVRVREATRAEYVVVMDRQGVRSHTDPERIGEVVSTDPGQA 140

Query: 141 MRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALIS 200
+ G E M + GTLG SAR KVP+ D + VG VSVG DSV +RL + L +
Sbjct: 141 LAGREVMEIDDGTLGRSARGKVFLRDGDGEI-VGAVSVGIAYDSVRARLIHAIPGLFAYA 199

Query: 201 VLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVH 260
+ +G + + RR +R T L ++ L+ + A++ GI EGV+AL G + +
Sbjct: 200 GGALAVGALASWIISSRRVQRQTRDLAFSDIAGLLAEREAMLHGIREGVVALDRGGRVRL 259

Query: 261 NEQAQSMIG-AGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHPV----- 314
N++AQ ++G G GR+ E G+ + +A GR+ D V
Sbjct: 260 NDEAQRLLGIGGEAVGRSPDEALGA-----GRTADVLA--GRVTGTDLLTVRGQRV 308

Query: 315 ----RRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDA 370
R D G V T+RDRT++ +L LDS R + ALRAQ HE ANR+HT GL++
Sbjct: 309 LVANRMPTDDGGAVATLRDRTLEQLGRELDSTRGLIDALRAQDHEHANRMHTLLGLEL 368

Query: 371 GRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEKGVSLRINSDTLI 430
DA EF+G++ + + I + +++ E+GV+LR++ T +
Sbjct: 369 EMYDDAVEFVGEVVGDRHVTAQI-TERIHDPLLAALLVGKATVAAERGVALRVSDRTRL 427

Query: 431 LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGV 490
+ DP + TI+GNL++NA+DAA AG A +E+ L + ++V D+GPGI
Sbjct: 428 PDRLVDPRLVTIVGNLVDNALDAA-AGTAHARVEVELRAEGRAATLTVRDTCGPI--AA 484

Query: 491 DVFATATQIGDSEDNERTH-GHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLP 547
D G S H GIGL L R LA GG + GA F V LP
Sbjct: 485 DHRELVAAGWSTKEPPAHRERGIGLFLVRLAERQGGSA-TVGEAYGGGAEFVVVLP 541

>gi|29828972|ref|NP_823606.1| putative two-component system sensor kinase [Strepto
avermitilis MA-4680]
gi|29606077|dbj|BAC70141.1| putative two-component system sensor kinase [Streptom
avermitilis MA-4680]
Length = 575

Score = 213 bits (541), Expect = 1e-53
Identities = 178/538 (33%), Positives = 275/538 (51%), Gaps = 37/538 (6%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMDQMKEAHTALSIGRSVASNPQIREEVALDTQ 80
+++L++QV+ A V + TG+F + Q+ +A AL+I ++ A+ PQI E+
Sbjct: 20 SQVLLMQVSIAGVAVLATGLFLAPLSAQQLDDQAMRRALAIQAQTTAAQPQIAEDF----- 74

Query: 81 TGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEEA 140

PS G +Q A+ + +GA +VV+ + G+R SH D ++G+ VST A
Sbjct: 75 QATRPV---GGPVQTEAERIRKASGA EYVVVMNMDGVRWSHTDPTQIGKVVSTDPREA 130
Query: 141 MRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALIS 200
+ G++ M + CTLG SAR KVP+ D + VG VSVG E DSV +RL + + L +
Sbjct: 131 LAGKDVMOIDNGTLGRSARGKVPLRNADDKI-VGAVSVGIEYDSVRARLILAIPGLFAYA 189
Query: 201 VLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVH 260
+ IG A + RR +R T L ++ L+ + A++ I EGV+AL G + +
Sbjct: 190 GAALAIGAVAAYLISRRVQRQTRDLAFSDISALLAEREAMLHSIREGVVALDRGGRVRL 249
Query: 261 NEQAQSMIGAGPMS-GRTLKXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHPVR---- 315
N++AQ ++G + G++L + G+ + +A GR+ D VR
Sbjct: 250 NDEAQRLLGLDAEAGQSLDDTLGP-----GRTTDVLA--GRVTGTDLLTVRGQRV 298
Query: 316 -----RGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDA 370
D G V T+RDRT++ +L LDS R + ALRAQ HE ANR+HT GL++
Sbjct: 299 LVANRMPTDDGGAVATLRDRTELEQLGRELDSTRGLIDALRAQDHEHANRMHTLLGLLEL 358
Query: 371 GRVHDAAEFLGDISRNGGQSHPLIGSAHLNXXXXXXXXXXXXXXXXXKGVSLRINSDTLI 430
DA EF+G++ + + + + + E+GV+L I+ TL+
Sbjct: 359 DMYDDAVEFVGEVVGDRHTTAEQV-TEKIHDPLLAALLVGKATVAAERGVALWISDRTL 417
Query: 431 LGTVKDFEDVATILGNLINNAIDA AVAGEAPRWIELTMDADTLVISVADSGPGIPEGV 490
+ DP + T++GNL++NA+D AVAG +E+ L + T V+ V D+GPGIP V
Sbjct: 418 PDRLIDPRGLVTVVGNLVDNALD-AVAGTPHARVEVELRAEGRTTVLRVRDTGPGIP--V 474
Query: 491 DVFATATQIGDSEDNERTHG-HGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLP 547
+ G + HG GIGL L R LA GG V D GA F V LP
Sbjct: 475 ERRELIFTDGTWTKKPPAHGKRGIGLSLVRRLAERQGG SARV-DEADGGGAFTVVLP 531

>gi|15616401|ref|NP_244706.1| two-component sensor histidine kinase [Bacillus halo
gi|21362444|sp|Q9RC53|CITS_BACHD Sensor protein cits
gi|25298484|pir|G84129 two-component sensor histidine kinase cits [imported] - B
halodurans (strain C-125)
gi|5822800|dbj|BAA83946.1| CITS [Bacillus halodurans]
gi|10176464|dbj|BAB07558.1| two-component sensor histidine kinase [Bacillus halod
Length = 538

Score = 172 bits (437), Expect = 1e-41

Identities = 144/532 (27%), Positives = 260/532 (48%), Gaps = 33/532 (6%)

Query: 31 VALVVAICTGIFAVLMMDQ---MKTEAHTALSIGRSVASNPQIREVALDTQTGANPS 86
+AL++ + V + +Q ++ + ALS+ ++VA P++RE +
Sbjct: 18 IALLIIAMFVLLGVFLNEQYARTLEEQMGGERALSVAQAVALIPELREAFS----- 67
Query: 87 AEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--STSFEAAMRGE 144
E D IQ +A++ TGA F+V+ + IR +HP ER+G+++ + A + GE
Sbjct: 68 -AERPDEIIQPIAESIRVETGAEFIVVGNITDLIRYAHPLPERIGQRMVGGDNERALVHGE 126
Query: 145 ETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGI 204
++ G+LG S R KVP+F + + +G VSVG F + + + L A+ I V+ +
Sbjct: 127 SYVSKAVGSLGPSIRGKVPVFDNGKI-IGIVSVGFLMEDIQQVIGERLIAMWQIVVVIM 185
Query: 205 LIGVGAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQA 264
++G+ + ++ TLGL+PEE+ Q + A++ I EGV+A++ G + + N+ A
Sbjct: 186 ILGLMGTWLVANTVKKATLGLPEEIGQQFQQKEAILQSIHEGVIAVNKEGKVTLFNQAA 245

Query: 265 QSMIG---AGPMSGRTLKEXXXXXXXXXXXXXX--HGQHPETVAHNGRILVLD FHPVRRGD 318
+ GR + + GQ+ + + + ++ P+
Sbjct: 246 MKYVDPELDKEDVLGRHVTDLVKHTRLPEVLQVKGQYDQELRIGDKQAVVNRVPIYYDH 305

Query: 319 QDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDHAAE 378
+ +G V T RDR +I +LSE L +V+ ALRAQ HEF+N+++T +G + G++ +A +
Sbjct: 306 EIVGAVATFRDRNEIKKLSEELTNVKNYADALRAQTHEFSNKLNTISGFLQLGKIDEAVD 365

Query: 379 FLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEKGVSLRINSDTLILGTVKD-- 436
F+ R Q +N+ E G+ + I+ + +L +++
Sbjct: 366 FIOK-ERKIQQEWIHFFIERVNDPTVSAVLLGKISQAQELGIDVDIDPSSQLLTPLQERQ 424

Query: 437 PEDVATILGNLINNAIDAABA-GEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFAT 495
E + T++GNL+ NA DA +A G + I ++ D D + V D+GPGIP + +
Sbjct: 425 QELLVTMIGNLLENAFDALLASGIENKKIYISFTDMGDDFIFEVEDNGPGIPP--QLMES 482

Query: 496 ATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTSQDGA VFGVKLP 547
+ G S E TH G GL L + GG ++ ++ G GA F + +P
Sbjct: 483 IFEEGFST-KEGTH-RGFGLALVKKAVHELGAIF-LEEGELGGACFVLTIP 531

>gi|15640810|ref|NP_230440.1| sensor kinase cita [Vibrio cholerae O1 biovar eltor
gi|11277517|pir|C82280 sensor kinase cita VC0791 [imported] - Vibrio cholerae (N16961 serogroup O1)
gi|9655240|gb|AAF93956.1| sensor kinase cita [Vibrio cholerae O1 biovar eltor str
Length = 565

Score = 167 bits (424), Expect = 4e-40
Identities = 154/569 (27%), Positives = 255/569 (44%), Gaps = 44/569 (7%)

Query: 1 MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALS 60
M + + + + K + F R+ + VA V + + + + G F + + + + AL
Sbjct: 1 MKISLAQLHTKVCQTLSPQQRVGALLVAMVVIQLSLVAGFFHQTLSLQDQISTKALI 60

Query: 61 IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVI TDGLGIR 120
R +A++P + + L Q N AE +QA + A F+VI D GIR
Sbjct: 61 QAREIATDPNL---IVLIQQ---NRLAE-----VQAKIDRLQRISDANFIVIGDANGIR 108

Query: 121 LSHPDEERLG--EQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSV 178
++HPDE+++G Q S A GE + + G+LG + R K I AP + +G VSV
Sbjct: 109 IAHPEQKIGLPMQGGDSRRALKEGEYYTSTQKGS LGWAIRGKAAIVAPSGEI-LGVVSV 167

Query: 179 GFERDSVYSRLPMFLAALALISVLGILIGVGVMGMRRRWERVTLGLQPEELVTLVQNQT 238
G+ D++ S L ++ + +L +L+ A R ++ ++PEE+ + Q
Sbjct: 168 GYLLDNISSWLRVYSYPVIFTVLLMLLSALGAWIFTRHIKQMFNMEPEEIAMNLNLQQ 227

Query: 239 AVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGP---MSGRTLKEXXXXXXXXXXXXXXH- 293
+++ + EG++A+S G I N +A +++G + GR ++E
Sbjct: 228 SILQSVYEGIVAISLKGEILSVNAKALNILGLAHQPTHIGRNVQEFITPTCFMGASPF 287

Query: 294 -----GQHPETVAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVR 344
Q E ++ NG L + P+ G Q +G+VV+ R R D L+ +L +R
Sbjct: 288 GKLAQQNRVSQQDELISCNGETLVANRVPINSGQQQIGWVVSFRRRNDFNLTLSQLTQIR 347

Query: 345 TMTHALRAQRHEFANRIHTATGLIDAGRVDHAAEFLGDISRNGGQSHPLIGSAHLNEXXX 404
LR HEFANR+ T GLI G +A + I R + LI
Sbjct: 348 QHNDNLRVMSHEFANRLSTIGGLIQIGAYDEAVK---TIRRETAEQQQLIDFIAQT FHPK 404

Query: 405 XXXXXXXXXXXXXKEKGVSLRINSDTLILGTVKDPE-----DVATILGNLINNAIDAAG- 458

K + L + D L ++P+ ++A +LGNL++NA +A +
Sbjct: 405 VIAGLLLGKYSRAKELGLCLFDFPLS-HLHQEPQCMTSDELA AVLGNLLDNAFEATLKNP 463
Query: 459 EAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLK 518
+ + I L L D+ LVI VAD+G GI D+ T G S N+ GHGIGL L
Sbjct: 464 HSNKTIISLLTNGAELVIEVADNGIGI--SADIAQTLEFLKGVSSKNQ--EGHGIGLYLV 519
Query: 519 RALARSHGGDVWVIDRGTEGDGAVFGVKLP 547
G + +ID G +F + +P
Sbjct: 520 HQFVTQAHGSI-LIDSAEPQGTIFSIFIP 547

>gi|29829358|ref|NP_823992.1| putative two-component system sensor kinase [Strepto
avermitilis MA-4680]
gi|29606465|dbj|BAC70527.1| putative two-component system sensor kinase [Streptom
avermitilis MA-4680]
Length = 565

Score = 162 bits (409), Expect = 2e-38
Identities = 152/537 (28%), Positives = 248/537 (46%), Gaps = 27/537 (5%)

Query: 19 PATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVALD 78
A ++ +Q +A++VA V Q + A +++ RSVA P +R +
Sbjct: 12 LAGQLFAMQAVLIAVLVAGYALFTYVSDRSQAEAAARRQTMAVARSVADAPSVRAAIR- 70
Query: 79 TQTGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSE 138
++PSA +Q A TG FV I + GIR +HP+ + +GE+
Sbjct: 71 ----SDPSAA-----LQPYALQVQRHTGVDFVTIMNPRGIRWTHPNPDLIGERFLGHTT 120
Query: 139 AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALAL 198
A++GE TGTLG S RA PI D + +G VS G + +++ R+ + AL
Sbjct: 121 RALKGESFTETYTGTLGPSVRAVTPI--RDGTRIIGLVSAIKVEAITKRVQDQVTALIG 178
Query: 199 ISVLGILIGVGVAMGMRRRWERVTGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIG 258
++ + +G + R R T G+ EL + A + + EG+L L +
Sbjct: 179 VAAGALTGGIGTYVINARLRRSTHGMNAEELSRMHDYHQAALHAVREGLLMLDGGQFRVA 238
Query: 259 VHNEQAQSMIG-AGFMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAH--NGRILYLDPHFVR 315
+ N+ + ++G G + GR++ E + H R+L ++ PV
Sbjct: 239 LINDGGRELLGVTGDVIGRSVAELGLPAALTGALLSAEPRVDEVHLTAARVLVNTSPVS 298
Query: 316 RGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVD 375
G++ G VVT+RD T++ L LDS R T ALR+Q HE ANR+HT LI+ GR +
Sbjct: 299 GGERR-GTVVTLRDVTELQSLMGELDSERGFTTALRSQAHEAANRLHTTVVSLIELGRAEE 357
Query: 376 AAEF-LGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKGVSLRINSDTLILGTV 434
A +F ++ + ++ + ++E E+GV L ++ ++ + +
Sbjct: 358 AVDFATAELELAQALTDHVVSAA--VSEPVLALLLGKAAQANERGVELLVSEESALDDGL 415
Query: 435 KDP---EDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGV 490
P D+ TILGNLI+NA+DAA R + +T+ DA LV+ VAD+G G+
Sbjct: 416 LPPSLPARDLVITILGNLIDNAVDAAQGS MRAR-VTVTVFTDASGLVLRVADTGAGVDPAY 474
Query: 491 DVFATATQIGDSEDNERTHGHGIGLKLRLALARSHGGDVWVIDRGTEGDGAVFGVKLP 547
A + ++ + G G+GL L R H G + V + GA F V+LP
Sbjct: 475 -AEAVFQRGWSTKPATASGGRGLGLALVRQAVARHEGKLTVAE-ADGGGAEEFVRLP 529

>gi|21398877|ref|NP_654862.1| HATPase_c, Histidine kinase-, DNA gyrase B-, phytoch
ATPase [Bacillus anthracis A2012]
gi|30261052|ref|NP_843429.1| sensor histidine kinase [Bacillus anthracis str. Ame
gi|30254666|gb|AAP24915.1| sensor histidine kinase [Bacillus anthracis str. Ames]
Length = 529

Score = 160 bits (405), Expect = 7e-38
Identities = 141/543 (25%), Positives = 244/543 (44%), Gaps = 33/543 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMDQMKEAHTALSIGRSVASNPQIREEVA 76
+ T+I+ + +A+ VV+ GIF+ K+ E AL +S++ P I+E A
Sbjct: 7 VSLQTKIVSLIILFVVLALLAGIFVYIQSVDTKROVEQLALQTAKSLSFMPAIKE--A 64

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVST- 135
N +IQ++A+ E+ GA +V++ D G+ SH + E +G + +
Sbjct: 65 FQNNNEHKN-----NIQSI AEQVREQAGADYVIVEDRYGVMSHNSSELIGTKNNNP 115

Query: 136 -SFEAAMRGEETMAWETGTLGASARAKVPIFAP--DSSVPVGEVSVGFERDSVYSRLMP 192
++EA G GT + AK PI D VG V+V F + S +
Sbjct: 116 YNYEALTFGGYTYLEGNGTSSPALMAKAPIIVHNGDYDQVVGVTVEFLIKGIESNILSR 175

Query: 193 LAALALISVLGILIGVGVAMGMRWRERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252
+ L S+ +L+G+ + + R + TLGL+P E+ L + ++A++ I EG++A+
Sbjct: 176 TKEIILFSLAVLLVGIVGGILLARSIRKDTLGLSPNEIAALYRERSAILLSIKEGIIAID 235

Query: 253 PNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHG-QHPETVAHNGRILYLD 311
NG I + N A+ M+ ++G +++ ++ + +A ++ L+
Sbjct: 236 RNGFITMTNTSAEEMLH--VNGDYMQQHISKVLPEFHMERVLENDQEIAFQDKVFILNM 292

Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
P+ + +G V + RD+T++ L + VR + LRAQ HEF N++ +GL+ G
Sbjct: 293 TPILENNNTVGVVCSFRDKTELQNLVNTISEVRKYSDDLRAQTHEFTNKLFVLSGLLQLG 352

Query: 372 RVHDAAEFLGDISR-NGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLI 430
+A EF+ S + Q+H L H + EK + I D+
Sbjct: 353 HYREAIEFIQGESNIHQSNHILFHQIH--DAKVQAILLGKIGTASEKKIDPFHIEGDS-A 409

Query: 431 LGTVKQPEDVA---TILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIP 487
L + D V+ TILGN+I+NA D AV+ + + + D +V V D G GIP
Sbjct: 410 LHPLPDHIKVSHLITILGNIIDNAFD-AVSEREEKNVSFFVTDIGHDIVFEVIDRGIGIP 468

Query: 488 EGVDFVATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLP 547
+ T Q G S + + G GL + + G + I GA+F + LP
Sbjct: 469 --AEKITTIFQKGFS---TKGNNGYGLANVKEMVDVLEGTI-EIQNERNGGAIFTIYLP 522

Query: 548 GVM 550
+
Sbjct: 523 KTL 525

>gi|16060204|ref|NP_391030.1| similar to two-component sensor histidine kinase [Yu
subtilis]
gi|7428875|pir|A70009 two-component sensor histidine kinase homolog yufL - Bacil
subtilis
gi|1934809|emb|CAP07946.1| unknown [Bacillus subtilis]
gi|2635648|emb|CAP15141.1| yufL [Bacillus subtilis subsp. subtilis str. 168]
Length = 533

Score = 159 bits (402), Expect = 1e-37

Identities = 133/529 (25%), Positives = 245/528 (46%), Gaps = 27/528 (5%)

Query: 33 LVVAICTGIFAVLMDQMKTEAHTALSIGRSVASNPQIREVALDTQTGANPSAEELAD 92
L + +C + L++ A+ T + A+ Q E VA T A + +
Sbjct: 11 LTIFVCIVVLIALLITFTVGAQTTKRIRDQEKATALQTAEMVAEAPMTAAALESKG-KQ 69

Query: 93 GDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEA-AMRGEETMAWET 151
++Q+ + + TG FVV+ D GIR +HPD ++G++ E+ ++G ++ +
Sbjct: 70 KELQSYTKRVQKITGTEFVVVMDMNGIRKTHPDPSKIGKKFRGGDESEVLKGVHISTAS 129

Query: 152 GTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVA 211
GTLG S RA VP++A + VG V+VG + + + L L I + I +GV A
Sbjct: 130 GTLGKSQRAFPVVAENGK-QVGAVAVGITVNEIDEVISHSLRPLYFIICVSIFVGVIGA 188

Query: 212 MGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSM---- 267
+ + R + + GL+P E+ TL++ ++A+++ EG+LA+ +G I + N +A+ +
Sbjct: 189 VIVARTVKNIMYCLEPYEATLLEERSAMLESTKEGILAVDEHGKIKLANAEAKRLFVKM 248

Query: 268 -IGAGPMSGRTLKEXXXXXXXXXXXXXXHGQHP--ETVAHNGRILYLDHFHVRGQDQDLGY 323
I P+ + + P V NG L + P++ Q +G
Sbjct: 249 GINTNPIDQDV--DDILPKSRLKKVIETKKPLQDRDVRINGLGLVFNVPVPIQLKGQTVGA 306

Query: 324 VVTIRDRTDIELSERLDSVRTMTALRAQRHEFANRIHTATGLIDAGRVDAAEFLGDI 383
+ T RD+T++ L+E+L V+ +ALRAQ HEF N++H GL+ D +++ DI
Sbjct: 307 IATFRDKTEVKHLAEQLSGVKMYANALRAQSHEFTMNLHVILGLVQLKEYDDLGDYIKDI 366

Query: 384 S-RNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLILGTVKDP---ED 439
+ + ++ +I + E+G +L I + +I DP +
Sbjct: 367 AIQQKSETSEIIND--VKSSVLGFLGKQSFIREQGANLDIECNGVI-PNAADPSVIHE 423

Query: 440 VATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQI 499
+ TI+GNLNN +D AVA + I +++ L I + D+G G+ E ++
Sbjct: 424 LITIIGNLINNGLD-AVADMPKKQITMSMRFHNSILDIITDTGAGMSE-----EDQAKV 477

Query: 500 GDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKLP 547
+ + + G GL + + G + ++ +G F +++P
Sbjct: 478 FEQGYSTKGXNRGFGLYFTQQSIENLKGQM-ILTSEKNEGTTFSIRIP 524

>gi|30019091|ref|NP_830722.1| Two-component sensor kinase citS [Bacillus cereus AT
gi|29894634|gb|AAP07923.1| Two-component sensor kinase citS [Bacillus cereus ATCC
Length = 538

Score = 158 bits (400), Expect = 2e-37

Identities = 141/543 (25%), Positives = 238/543 (43%), Gaps = 31/543 (5%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMDQMKTEAHTALSIGRSVASNPQIREEVA 76
+ T+I+ + + + VV + GIF + K + E AL +S++ P I+E
Sbjct: 7 VSLQTKIVSLIITLILFVLLLAGIFVYIQSVDTKHQVEQLALQTAKSLSFMPAIKEAF- 65

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVST- 135
Q + S IQ++A+ E+ GA +V++ D G+ SH + E +G + +
Sbjct: 66 ---QNNEHKST-----IQSIAEQVREQAGADYVIVEDRYGVMYSHSNSELIGTKSNNP 115

Query: 136 -SFEAAMRGEETMAWETGTLGASARAKVPIFAP--DSSVPVGEVSVGFERDSVYSRLPMF 192
++EA G GT G + AK PI D VG V+V F + S +
Sbjct: 116 YNYEALTFGGYYTLEGNGTSGPALMAKAPIIVHNGDYDQVVGVTVEFLIKGIESNILSR 175

Query: 193 LAALALISVLGILIGVGVAAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252

```

      + L S+ +L G+ + + R + TLGL+P E+ I + ++A++ I EG++A+
Sbjct: 176 TKEIILFSLGVLLAGIVGGILLARSIRKDTLGLPEPNEIAALYRERSAILLSIKEGIIAID 235

Query: 253 PNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHCQHPETVAHNGRILYLDHFH 312
      NG I + N A+ M+ + + +A ++ L+
Sbjct: 236 QNGFITMMNTSAERMLHVN--DDYMQQHISKVLPNFMERVLETDQEIAFQDKVFILNMT 293

Query: 313 PVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGR 372
      P+ + +G V + RD+T++ L + VR + LRAQ HEF N++ +GL+ G+
Sbjct: 294 PILENNSTVGVCVCSFRDKTELQNLVNTISEVRKYSEDLRAQTHEFTNKLFVLSGLLQLGQ 353

Query: 373 VHDAAEFLGDISR-NGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKEGVSLRINSDTLIL 431
      +A EF+ S + Q+H L H + EK + I D+ L
Sbjct: 354 YKEAIEFIQQESNIHQSNHILFHQIH--DAKVQAILLGKIGTASEKKIDFHIEGDS-AL 410

Query: 432 GTVKDPEDVA---TILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
      + D V+ TILGN+I+NA D AV+ + + + D +V V DSG GIP
Sbjct: 411 HPLPDHIKVSHLITILGNIIDNAFD-AVSEEREKSVSFFVTDIGRDI VFEVIDSGIGIPA 469

Query: 489 GVDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLPG 548
      T I + + G GL + + CG + I GA+F + LP
Sbjct: 470 -----EKITTIFRKGFSTKGTDRGYGLANMKEMVDLLGGTI-EIQNEKNGGAIFTIYLPK 523

Query: 549 VME 551
      +E
Sbjct: 524 NIE 526

```

```

>gi|15800334|ref|NP_286346.1| putative sensor-type protein [Escherichia coli O157:
gi|15829912|ref|NP_308685.1| putative sensor-type protein [Escherichia coli O157:
gi|25298480|pir|B90711| probable sensor-type protein [imported] - Escherichia col
O157:H7, substrain RIMD 0509952)
gi|25298485|pir|F95561| probable sensor-type protein cita [imported] - Escherichi
(strain O157:H7, substrain EDL933)
gi|12513518|gb|AAG54954.1| putative sensor-type protein [Escherichia coli O157:H7
gi|13360116|dbj|BAB34081.1| putative sensor-type protein [Escherichia coli O157:H
Length = 552

```

Score = 156 bits (395), Expect = 9e-37
Identities = 146/559 (26%), Positives = 246/559 (44%), Gaps = 44/559 (7%)

```

Query: 9 KNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASN 68
      K F + F RI ++ + V+A F D + A++ + +ASN
Sbjct: 8 KQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTASFEDYLT LHVRDMAMNQAKIIASN 67

Query: 69 PQIREEVALDTQTGANPSABELADGDIQAVAQAANE---RTGALFVVITDGLGIRLSHPD 125
      + EV D + +A AN+ T +VVI D IRL HF+
Sbjct: 68 DSVISEVKTR-----DYKRLATIANKLQRDTDFDYVVIGDRHSIRLYHPN 112

Query: 126 EERLGEQVSTSFEAAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDS 184
      E++G + + + A+ +GE G++G + RAK PIF D V +G VS+G+
Sbjct: 113 PEKICYPMQFTKQGALEKGESYFITGKSGMGMAMRAKTPIFDDDGKV-IGVVSIGYLVSK 171

Query: 185 VYSRLPMFLAALA--LISVLGILIGVGAMGMRRRWERTLGLQPEELVTLVQNQTAVID 242
      + S FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+
Sbjct: 172 IDSWRAEFLLPMAGVFVLLGILMLLSWFLAAHIR--RQMMGMEPKQIARVVRQQEALFS 229

Query: 243 GIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXXHCQHP 298
      + EG++A+ P+G I N A+ M+G G+ + E + +

```

Sbjct: 230 SVYEGLIAVDPHGYITAINRNARKMLGLSSPGRQWLKPIAEVVRPADFFTEQIDEKRQD 289
Query: 299 TVAH-NGRILYLDHFVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEF 357
VA+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE
Sbjct: 290 VVANFNGLSVIANREAIRSGDDLLGAIISFRSKDEISTLNAQLTQIKQYVESLRTL RHEH 349
Query: 358 ANRIHTATGLIDAGRVDAAEFGLDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXXX 415
N + T GL+ ++ + L + LI S +
Sbjct: 350 LNMWSTLNGLL---QMKEYDRVLAMVQGESQAQQQLIDSLREAFADRQVAGLLFGKVQRA 406
Query: 416 XEKGVSRLI--NSDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDA 472
E G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+
Sbjct: 407 RELGLKMIIVPGSQLSGLPPGLDSTEFAAIVGNLLDNAFEASLRSDEGNKIVELFLSDEG 466
Query: 473 DTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARLSHGSDVW 530
D +VI VAD G G+PE + +F E E HGIGL L + GG V
Sbjct: 467 DDVVEIADQGCVPESLRDKIFEQGVSTRADEPGE---HGIGLYLIASVYTRCGG-VI 521
Query: 531 VIDRGTEGAVFGVKLPV 549
++ G +F + +P V
Sbjct: 522 TLEDNDPCGTLFSIYIPKV 540

>gi|30260717|ref|NP_843094.1| sensor histidine kinase [Bacillus anthracis str. Ame
gi|30254085|gb|AAP24580.1| sensor histidine kinase [Bacillus anthracis str. Ames]
Length = 536

Score = 155 bits (391), Expect = 2e-36
Identities = 133/543 (24%), Positives = 256/543 (47%), Gaps = 32/543 (5%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
++ RI + A + +V+ + + +F ++ + ++ + AL + ++VA+ P+I+E A
Sbjct: 8 LKLQPRITLTISALILVVLMLTSYLFYYILSETVBEQIGKRALHVAKTVAAIPEIKE--A 65
Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--S 134
T+ NP++ IQ +A+ T A F+V+ + GIR +HP+ +++GE +
Sbjct: 66 FQTE---NPAS-----IIQPIAERIRMDTEADFI VVGNKEGIRYAHPERDKIGEAMIGG 116
Query: 135 TSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
+ + G+ ++ TG+LG S R KVPI ++ + +G VSVGF D ++ + ++
Sbjct: 117 DNKGVLLLEGKSYVSKATGSLGPSLRGKVPIRNQENI-IGVVS VGFMSDDIHGAVEVYVK 175
Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
+ I+++G+LIGV ++ + +R+ G++PEE+ +L + + VI + EG++ + N
Sbjct: 176 RVFWITIIIGLLIGVIGSIYLAGSIKRMFMGEPEEISSLYEEHSTVIQSVREGIIVIDQN 235
Query: 255 GTIGVHNEQAQSMIGAGPMS---GRTLKEXXXXXXXXXXXXXXHC--QHPETVAHNGRILYL 309
G I + N+ A ++ G + + G Q + G+ +
Sbjct: 236 GMISLVNQAAVDILALDEQRNIIGEFILDIIPNSTILDVLQTGEEQFDRQLNIKQQAVIA 295
Query: 310 DFHFVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ P++ ++ G V ++R +++ +L+ L + T ALRAQ HE+ N ++T +GLI
Sbjct: 296 NRLPIKVIQKVTVGVVSSLRLKSEMDQLTAE LSQTKQYTEALRAQTHEYNNLLYTL SGLIQ 355
Query: 370 AGRVHDAAEFGLDISRNGGQSHPLIG--SAHLNEXXXXXXXXXXXXXXKEKGVSLRINS 427
DA E I + + + E + ++ +
Sbjct: 356 LELYEDALEL---IHKETAVYQDFVQFIMKRIQNPWLGGILIGFYNRARELKIEFMLDRE 412
Query: 428 TLI--LGTVKDPEDVATILGNLINNAIDAAVAGEA-PRWIELTLMDDADTLVISVADSGP 484

+ + L + V +ILGNLI NA +A E + + + + D + +VI V DSG
Sbjct: 413 SSLDKLSPPIESNYVVSILGNLITNAFEAIERNEEHDKKVRMFVTDIGEEIVIEVEDSGQ 472
Query: 485 GIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGV 544
GI + V E +R G GL + L G + I++G GA+F +
Sbjct: 473 GIHDEVITSIFYKGFSTKEGEKR---GYGLAKVKELVEDLNGSI-AIEKGDLCGALFII 527
Query: 545 KLP 547
LP
Sbjct: 528 ALP 530

>gi|16767554|ref|NP_463169.1| sensory histidine kinase [Salmonella typhimurium LT2]
gi|16422866|gb|AA123128.1| sensory histidine kinase in two-component regulatory
DcuR [Salmonella typhimurium LT2]
Length = 543

Score = 154 bits (390), Expect = 4e-36
Identities = 143/547 (26%), Positives = 254/547 (46%), Gaps = 42/547 (7%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVA 76
++ T ++++ A + V+ + I+ + + AL++ RS+A +P +RE +
Sbjct: 15 MKLGGTTVILMVSAVLFVSVLVVHLYFSQISSMTRDALADKALAVARSLADSPAVREGLK 74
Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
P AE IQ +A+A ++ G LF+V+T+ GIR SHP+ +R+G+
Sbjct: 75 -----KPPAES----GIQTLAEAVSQHNGFLFIVVTNMQGIRYSHPETQRIGQPFKGD 123
Query: 136 SFEEAMRGEBTMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A++G+E +A G L + R P++ + +G V++G E V ++ +
Sbjct: 124 DILLALQKENVAINRGFLAKALRVFTPVY-DEHHRQIGVVAIGLELSHVTQQINNSRGS 182
Query: 196 LALISVLGILIGVGVMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G L+G+ * + +R+ GL+P E+ TL + + A++ I EGV+A+ +G
Sbjct: 183 IIWSILFGALVGLLGTALVKVLKRILFGLPEYISTLFEQRQAMLQSIKEGVIAVDDSG 242
Query: 256 TIGVHNEQAQSMIGAGPMSG----RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNIRILY 308
+ + N AQ+++ TL P E + GR+L
Sbjct: 243 EVTLINHAAQALLDYRKTQDDARLSTLSHAWSQVVDISEVLRDGTFRRDEEIIIVKGRLLL 302
Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
++ PVR + +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 VNTVPVRSNGEIIIGAISTFRDKTEVRQLMQRLDGMVNYADALRERSHEFMNKLHVILGLL 362
Query: 369 DAGRVHDAEFLGDISRGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEGVSLRINSDT 428
++ + N + L+ + + G SL I+SD+
Sbjct: 363 HLKSYKQLEAYIIKTANNYQEEIGLL-LGKIKSPIIAGFLLSKITRASDFGHSIVISSDS 421
Query: 429 LILGTVKDPEDVATI---LGNLINNAIDA AVAGEAPRWIBLTLMDDADTLVISVADSGP 484
+ + ED T+ LGNLI NA++ A++ E+ I ++L L V+D GP
Sbjct: 422 QLPDN--NNEDQVTVLITALGNLIENALE-ALSQESGGEISVSLHYRHGWLHCEVSDDGP 478
Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAV- 541
GI PE ++ +F S+ ER G+GL L + + GG VI +E G
Sbjct: 479 GIEPERIEAIFKEGVS---SKGAER---GVGLALVKQVEALGG---VISVESEPGIFT 529
Query: 542 -FGVKLP 547
F V+LP
Sbjct: 529 QFFVQLP 535

>gi|16128602|ref|NP_415152.1| putative sensor-type protein [Escherichia coli K12]
gi|2500761|sp|P77510|DPIB_ECOLI Sensor kinase dpiB (Sensor kinase cita)
gi|7428878|pir|A64796 signal-transducing histidine kinase homolog b0619 - Escher
coli (strain K-12)
gi|1778536|gb|AAB40819.1| sensor kinase Cita homolog [Escherichia coli]
gi|1786837|gb|AAC73720.1| putative sensor-type protein [Escherichia coli K12]
gi|4062236|dbj|BAA35255.1| Sensor kinase Cita [Escherichia coli K12]
gi|4062242|dbj|BAA35261.1| Sensor kinase Cita [Escherichia coli K12]
Length = 552

Score = 153 bits (387), Expect = 7e-36

Identities = 145/559 (25%), Positives = 245/559 (43%), Gaps = 44/559 (7%)

Query: 9 KNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASN 68
K F + F RI ++ + V+A F D + A++ + +ASN
Sbjct: 8 KQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTASFEDYLTlhVRDMAMNQAKIIASN 67
Query: 69 PQIRBEVALDTQTGANPSAEELADGDIQAVAOAANE---RTGALFVVITDGLGIRLSHPD 125
+ V D + +A AN+ T +VVI D IRL HP+
Sbjct: 68 DSVISAVKTR-----DYKRLATIANKLQRDITDFDYVVIGDRHSIRLYHPN 112
Query: 126 EERLGEQVSTSFEEAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDS 184
E++G + + + A+ +GE G++G + RAK PIF D V +G VS+G+
Sbjct: 113 PEKIGYPMQFTKQGALEKGESYFITGKSGMGMAMRAKTFIFDDDGKV-IGVVSIGYLVSK 171
Query: 185 VYSRLPMFLAALA--LISVLGILIGVGVMGMRWRVTLGLQPEELVTLVQNQTAVID 242
+ S FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+
Sbjct: 172 IDSWRAEFLLPAGVFVLLGILMLLSWFLAAHIR--RQMMGMEPKQIARVVRQREALFS 229
Query: 243 GIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXXEQHPE 298
+ EG++A+ P+G I N A+ M+G G+ + E + +
Sbjct: 230 SVYEGLIAVDPHGYITAINRNARKMLGLSSPGRQWLKPIVEVVRPADFFTEQIDEKRQD 289
Query: 299 TVAH-NGRILYLDHFHVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTALRAQRHEF 357
VA+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE
Sbjct: 290 VVANFNGLSVIANREAIRSGDDLLGAIISFRSKDEISTLNAQLTQIKQYVESLRTLREH 349
Query: 358 ANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXX 415
N + T GL+ ++ + L + LI S +
Sbjct: 350 LNWMSTLNGLL---QMKEYDRVLMVQGESQAQQQLIDSLREAFADRVAGLLFGKVQRA 406
Query: 416 XEKGVSRLRI--NSDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDA 472
E G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+
Sbjct: 407 RELGLKMIIVPGSQLSQLPPLDSTEFAAIVGNLLDNAFEASLRSDGKNKIVELFLSDEG 466
Query: 473 DTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVW 530
D +VI VAD G G+PE + +F E E HGIGL L + GG V
Sbjct: 467 DDVVIEVADQCGVPESLRDKIFEQGVSTRADEPGE---HGIGLYLIASVTRCGG-VI 521
Query: 531 VIDRGTEGAVFGVKLPGV 549
++ G +F + +P V
Sbjct: 522 TLEDNPPCGTLFSIYIPKV 540

>gi|16762986|ref|NP_458603.1| two-component sensor kinase [Salmonella enterica sub
serovar Typhi]

gi|29144473|ref|NP_807815.1| two-component sensor kinase [Salmonella enterica sub
serovar Typhi Ty2]
gi|25298489|pir|AH1023| two-component sensor kinase (EC 2.7.3.-) [imported] - Sal
enterica subsp. enterica serovar Typhi (strain CT18)
gi|16505293|emb|CAD09289.1| two-component sensor kinase [Salmonella enterica subs
serovar Typhi]
gi|29140111|gb|AA071675.1| two-component sensor kinase [Salmonella enterica subsp
serovar Typhi Ty2]
Length = 543

Score = 153 bits (387), Expect = 7e-36
Identities = 143/547 (26%), Positives = 254/547 (46%), Gaps = 42/547 (7%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVA 76
++ T ++++ A + V+ + I+ + + AL++ RS+A +P IRE +
Sbjct: 15 MKLGTTVILMVSAVLFSVLVVVHLIYFSQISSMTRDALADKALAVARSLADSPAIREGLK 74

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
P AE IQ +++A ++ G LF+V+T+ GIR SHP+ +R+G+
Sbjct: 75 -----KPPAES-----GIQPLSEAVSQHNGFLFIVVTNMQGIRYSHPETQRIGQPFKGD 123

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVFIAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A++G+E +A G L + R P++ + +G V++G E V ++ +
Sbjct: 124 DILLALOGKENVAINRGFLAKALRVFTFVY-DEHHRQIGVVAIGLELSHVTQQINNSRGS 182

Query: 196 LALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G L+G+ + + +R+ GL+P E+ TL + + A++ I EGV+A+ +G
Sbjct: 183 IIWSILFGALVGLLGTXYALVKVLKRILFGLPEYEISTLFPEQRQAMLQSIKEGVIAVDGSG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG---RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNGRILY 308
+ + N AQ+++ TL P E + GR+L
Sbjct: 243 EVTLINHAAQALLDYRKTDQDARLSTLSHAWPQVVDISEVLRDGTFRRDEEIIVKGRLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
++ FVR + +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 VNTVPVRSNGEIIIGAISTFRDKTEVRQLMQRLDGMVNYADALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSOT 428
++ + N + L+ + + G SL I+SD+
Sbjct: 363 HLKSYKQLEAYIIKTANNYQEEIGLL-LGKIKSPIIAGFLLSKITRASDFGHSLSVSSDS 421

Query: 429 LILGTVKDPEDVATI---LGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGP 484
+ + ED T+ LGNLI NA++ A++ E+ I ++L L V+D GP
Sbjct: 422 QLPDN--NNEDQVTVLITALGNLIENALE-ALSQESGGEISVSLHYRHGWLHCEVSDDGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEGAV- 541
GI PE ++ +F S+ ER G+GL L + + GG VI +E G
Sbjct: 479 GIEPERIEAIFKGVGS---SKGAER---GVGLALVKQQVEALGG---VISVESEPGIFT 528

Query: 542 -FGVKLP 547
F V+LP
Sbjct: 529 QFFVQLP 535

>gi|26246600|ref|NP_752639.1| Sensor kinase dpiB [Escherichia coli CFT073]
gi|26106999|gb|AA079183.1| Sensor kinase dpiB [Escherichia coli CFT073]
Length = 572

Score = 153 bits (386), Expect = 9e-36

Identities = 145/556 (26%), Positives = 242/556 (43%), Gaps = 38/556 (6%)

Query: 9 KNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMDQMKTEAHTALSIGRSVASN 68
K F + F RI ++ + V+A F D + A++ + +ASN
Sbjct: 28 KQFAFFQRLAFLRIFLLILVFSIFVIAALAQYFTASFEDYLTLLHVRDMAMNQAKIIASN 87

Query: 69 PQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEER 128
I V + LA +A T +VVI D IRL HP+ E+
Sbjct: 88 DSIIISAVK-----TRDYKRLA-----TIADKLQRDTDFDYVVIGDRHSIRLYHPNPEK 135

Query: 129 LGEQVSTSFEEAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYS 187
+G + + A+ +GE G++G + RAK PIF D V +G VS+G+ + S
Sbjct: 136 IGYPMQFTKPGALEKGESYFITGKGSIGMAMRAKTPIFDDDGKV-IGVVSIGYLVSKIDS 194

Query: 188 RLPFLAALA--LISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGID 245
FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+ +
Sbjct: 195 WRAEFLLPAGVFVLLGILMLLSWFLAAHIR--RQMMGMEPKQIARVVRQOEALFSSVY 252

Query: 246 EGVLAISFNGTIGVHNEQAQSMIGAGFMS---GRTLKEXXXXXXXXXXXHGXHPETVA 301
EG++A+ P+G I N A+ M+G G+ + E + + VA
Sbjct: 253 EGLIADVDPHYITAINRNARKMLGLSSPGRQWLKPIAEVVRPADFFTEQIDEKRQDVVA 312

Query: 302 H-NGRILYLDHFHVRGDDQLGYVVTIRDRDIELSERLDSVRTMTHALRAQRHEFANR 360
+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE N
Sbjct: 313 NFNGLSVIANREAIRSGDDLGAIIISFRSKDEISTLNAQLTQIKQYVBSLRTLREHLNW 372

Query: 361 IHTATGLIDAGRVHDAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXEXEK 418
+ T GL+ ++ + L + LI S + E
Sbjct: 373 MSTLNGLL---QMKEYDRVLAMVQGESQAQQQLIDSLREAFADRQVAGLLFGKVQRAREL 429

Query: 419 GVSLRI--NSDTLILGTVDKPEDVATILGNLINNAIDAAV-ACEAPRWIELTLMDDADTL 475
G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+ D +
Sbjct: 430 GLKMVIVPGSQLSQLPPGLDSTEFAAIVGNLLDNAFEASLRSDGNKSVELFLSDEGDDV 489

Query: 476 VISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVID 533
VI VAD G G+PE + +F E E HGIGL L + GG V ++
Sbjct: 490 VIEVADQCGVPESLRDKIFEQGVSTRADEPGE---HGIGLYLIASVYVTRCGG-VITLE 544

Query: 534 RGTEDGAVFGVKLPGV 549
G +F + +P V
Sbjct: 545 DNDFCGTLFSIYIPKV 560

>gi|15804717|ref|NP_290758.1| putative 2-component sensor protein [Escherichia coli EDL933]
gi|15834361|ref|NP_313134.1| DcuS; two-component sensor protein [Escherichia coli]
gi|16131951|ref|NP_418549.1| putative 2-component sensor protein [Escherichia coli]
gi|2506733|sp|P39272|DCUS_ECOLI Sensor protein dcuS
gi|7428874|pir|D65222 hypothetical 60.6 kD protein in dcuB-lysU intergenic region Escherichia coli (strain K-12)
gi|25298481|pir|C91267 two-component sensor protein DcuS ECs5107 [imported] - Es coli (strain O157:H7, substrain RIMD 0509952)
gi|25298486|pir|H86107 probable 2-component sensor protein yjdh [imported] - Es coli (strain O157:H7, substrain EDL933)
gi|1790567|gb|AAC77086.1| putative 2-component sensor protein [Escherichia coli K]
gi|12519101|gb|AAG59324.1| putative 2-component sensor protein [Escherichia coli EDL933]
gi|13364584|dbj|BAB38530.1| two-component sensor protein DcuS [Escherichia coli O length = 543

Score = 152 bits (384), Expect = 2e-35

Identities = 133/529 (25%), Positives = 242/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
++ +T ++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
Sbjct: 15 MKLSTTVILMVSAVLFSVLLVHLYFSQISDMTRDGLANKALAVARTLADSPEIRQGLQ 74

Query: 77 LDTQTGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPAQRIGQPFKGD 123

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
Sbjct: 124 DILKALNGEENVAINRGFLAQAALRVFTPIY-DENHKQIGVVAIGLELSRVTTQQINDSRWS 182

Query: 196 LALISVLGILIGVGVMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G+L+G+ + + +++ GL+P E+ TL + + A++ I EGV+A+ G
Sbjct: 183 IIWSVLFGMLVGLIGTCILVKVLKILFGLFYEISTLFEQRQAMLQSIKEGVVAVD DRG 242

Query: 256 TIGVENEQAQSMIGAGPMSG----RTLKEXXXXXXXXXXXXXXHCQHP---ETVAHNRIILY 308
+ + N+ AQ ++ TL P E + R+L
Sbjct: 243 EVTLINDAAQELLNRYKRSQDDEKLSTLSHSWSQVVDVSEVLRDGTFRRDEBITIKDRLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368
++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 INTVPVRSNGVIIGAISTFRDKTEVRKLMQRDLGLVNYADALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXXXXXKGVSLRINS 426
+++ + N + IGS + + G +L +NS
Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLLGKIKSPVIAGFLISKINRATDLGHTLIINS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLNNDAIDAAVAGEAPRWIELTLMDDADTLVISVADSGP 484
++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP
Sbjct: 420 ESQLPDSGSEDQVATLITLGNLIENALE-ALGPEPGGBISVTLMYRHGWLHCEVND DGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARSHGCDVWV 531
GI P+ +D +F SE G+GL L + + GG + V
Sbjct: 479 GIAPDKIDHIFDKGVSTKGSE-----RGVGLALVKQQVENLGGSIAV 520

>gi|536970|gb|AAA97025.1| ORF_f543 [Escherichia coli]
Length = 543

Score = 152 bits (384), Expect = 2e-35

Identities = 133/529 (25%), Positives = 242/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
++ +T ++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
Sbjct: 15 MKLSTTVILMVSAVLFSVLLVHLYFSQISDMTRDGLANKALAVARTLADSPEIRQGLQ 74

Query: 77 LDTQTGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPAQRIGQPFKGD 123

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
Sbjct: 124 DILKALNGEENVAINRGFLAQAALRVFTPIY-DENHKQIGVVAIGLELSRVTTQQINDSRWS 182

Query: 196 LALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
 + + G+L+G+ + + +++ GL+P E+ TL + + A++ I EGV+A+ G
 Sbjct: 183 IIWSVLFGMLVGLIGTCILVKVLKILFGLPEYELSTLFEQRQAMLQSIKEGVVAVDDRG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG----RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNGRILY 308
 + + N+ AQ ++ TL P E + R+L
 Sbjct: 243 EVTLINDAAQELLNYRKSQDDEKLSTLSHWSQVVDVSEVLRDGTTPRRDEEITIKDRLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRDIEELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368
 ++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
 Sbjct: 303 INTVPVRSNGVIIGAISTFRDKTEVRKLMQRLDGLVNYXDALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXKGVSLRINS 426
 +++ + N + IGS + + G +L +NS
 Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLLGKIKSPVIAGFLISKINRATDLGHTLILNS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTMDADTLVISVADSGP 484
 ++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP
 Sbjct: 420 ESQLPDSGSEDQVATLITTLGNLIENALE-ALGPEPGGEISVTLHYRHGWLHCEVNDDGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWV 531
 GI P+ +D +F SE G+GL L + + GG + V
 Sbjct: 479 GIAPDKIDHIFDKGVSTKGS-----RCVGLALVKQQVENLGGSIIV 520

>gi|24115306|ref|NP_709816.1| putative 2-component sensor protein [Shigella flexne
 gi|30064694|ref|NP_838865.1| putative 2-component sensor protein [Shigella flexne
 2457T]
 gi|28558086|sp|P59341|DCUS SHIFL Sensor protein dcus
 gi|24054605|gb|AA045523.1| putative 2-component sensor protein [Shigella flexneri
 gi|30042954|gb|AAP18676.1| putative 2-component sensor protein [Shigella flexneri
 2457T]
 Length = 543

Score = 152 bits (383), Expect = 2e-35
 Identities = 133/529 (25%), Positives = 242/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMDQMKTAEHTALSIGRSVASNPQIREEVA 76
 ++ +T ++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
 Sbjct: 15 MKLSTTVILMVS AVLF SVLLV VHLIYFSQISDMTRDGLANKALAVARTLADSPEIRQGLQ 74

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
 Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
 Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPEAQRIGQPFKGD 123

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
 A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
 Sbjct: 124 DILNALNGEENVAINRGFLAQAALRVFTPIY-DENHKQIGVVAIGLELSRVTTQINDSRWS 182

Query: 196 LALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
 + + G+L+G+ + + +++ GL+P E+ TL + + A++ I EGV+A+ G
 Sbjct: 183 IIWSVLFGMLVGLIGTCILVKVLKILFGLPEYELSTLFEQRQAMLQSIKEGVVAVDDRG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG----RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNGRILY 308
 + + N+ AQ ++ TL P E + R+L
 Sbjct: 243 EVTLINDAAQELLNYRKSQDDEKLSTLSHWSQVVDVSEVLRDGTTPRRDEEITIKDRLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRDIEELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368
 ++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+

Sbjct: 303 INTVPVRSNGVIGAISTRDKTEVRKLMQRLDGLVNYADALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXXXXXKGVSLRINS 426

+++ + N + IGS + + G +L +NS

Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLGKIKSPVIAGFLISKINRATDLGHTLILNS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGP 484

++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP

Sbjct: 420 ESQLPDSGSEDQVATLITLGNLIENALE-ALGPEPGGEISVTLHYRHGWLHCEVNDDGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVVW 531

GI P+ +D +F SE G+GL L + + GG + V

Sbjct: 479 GIAPDKIDHIFDKGVSTKGSE-----RGVGLALVKQVENLGGSIIV 520

>gi|27365978|ref|NP_761506.1| Signal transduction histidine kinase regulating citr
metabolism [Vibrio vulnificus CMCP6]

gi|27362178|gb|AA011033.1| Signal transduction histidine kinase regulating citrat
metabolism [Vibrio vulnificus CMCP6]

Length = 539

Score = 151 bits (381), Expect = 4e-35

Identities = 146/533 (27%), Positives = 238/533 (44%), Gaps = 41/533 (7%)

Query: 17 IRPATRILVIQVAT--VALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREE 74

I F R+LVI + + L++ + G F A L Q + E AL + R +A++ + E

Sbjct: 6 ISPRKRMLVIMTSLGLIELLILVAAG-FAYLKYSQ-BQEMGQKALGVARFLATSTTVIEL 63

Query: 75 VALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV- 133

+ E D Q + + GA F+V+ D GIRL HP +ERLG +

Sbjct: 64 I-----ENRDDVTYQOKFRELTQALGAFFIVVGDREGIRLIHPVDERLGLPMR 111

Query: 134 -STSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVFPVGEVSVGFERDSVYSRLPMF 192

+ A GE ++ G+LG S R K +F V +G VSVG+ D + R+ F

Sbjct: 112 GGDNARALEEGEAYISTARGSLGYSVRGKAAVFNSSAGEV-IGVVSVGYLLDRLQDRIEFP 170

Query: 193 LAALALISVLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252

L +++L + V+ R+++R LG +PEE+ L + I EGVL++

Sbjct: 171 AWFLIAMTLLVVAANALVSNYASRKQFRAILGFEPPEIGRLYGEILDVTMSTIKEGVLSID 230

Query: 253 PNGTIGVHNEQAQSMIGAGPMS--GRTLKEXXXXXXXXXXXXXXHQ--HPETVAHNGRILY 308

+G + N A ++G P + L + GQ H + N + L

Sbjct: 231 SSGVLRISINRSAAQILGLDPAQVLNKPFLSDALPASDLVRVLETGQEDHDIELYLNQKRLI 290

Query: 309 LDFHPVRRGDQDLGVVVTIRDRDIIELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368

+ PV + +G V + R R +I EL+E+L + LR+Q HE N+++T +GL+

Sbjct: 291 ANRSPVYVEGKIVGAVSSFRLRDEISELTEQLSQTKEYADLLRSQTHEHRNKLTISGLV 350

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXXXXKGVSLRINS 426

G + + +G + LI + + E G+ L +

Sbjct: 351 QMGELDAVQQLIG---QETAHYQGLIEFLRDTIKDPLVAGMLLGKTERARELGLELVVEE 407

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDA---AVAGE----APRWIELTLMDDADTLV 476

+ L +PED+ TILGNLI+NA DA A+A E + R IE+++ D ++

Sbjct: 408 GARLEPLSAWLNPEEDITLILGNLIDNAFDATMSAIAQEGNFARSRTIEVSISDPYCTEVI 467

Query: 477 ISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDV 529

+ V D G G+P+ F+T + ++ T G+GL L LA + G +

Sbjct: 468 LEVQDQGCGLPKQ---FSTEQLLEKGISSKATSTRGVGLYLVNQLAARYCGSI 517

>gi|26250939|ref|NP_756979.1| Sensor protein dcuS [Escherichia coli CFT073]
gi|29558085|sp|P59340|DCUS_ECOL6 Sensor protein dcuS
gi|26111371|gb|AAN83553.1| Sensor protein dcuS [Escherichia coli CFT073]
Length = 543

Score = 151 bits (381), Expect = 4e-35

Identities = 133/529 (25%), Positives = 241/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIRBEVA 76
++ +T ++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
Sbjct: 15 MKLSTTVILMVS AVLFSVLLVHLLIYFSQISDMTRDGLANKALAVARTLADSP EIRQLQ 74

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPEAQRIGQPFKGD 123

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
Sbjct: 124 DILKALNGEENVAINRGFLAQALRVFTPIY-DENHKQIGVVAIGLELSRVTTQINDSRWS 182

Query: 196 LALISVLGILIGVGVAMGMRWRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G+L+G+ + +++ GL+P E+ TL + + A++ I EGV+A+ G
Sbjct: 183 IIWSVLFGMLVGLIGTCILVNVLLKKILFGLPEYEISTLFEQRQAMLQSIKEGVVAVDDRG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG---RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNGRILY 309
+ + N+ AQ ++ TL P E + R+L
Sbjct: 243 EVTLLINDAAQELLNRYKRSQDDEKLSTLSHWSQVVDVSEVLRDGTPTRRDEEITIKORLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 INTVPVRSNGVTIIGAISTFRDKTEVRKLMQRLDGLVNYADALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXXXXXKEGVSLRINS 426
+++ + N + IGS + + G +L +NS
Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLLGKIKSPVIAGFLISKINRATDLGHTLILNS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGP 484
++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP
Sbjct: 420 ESQLPDSGSEDQVATLITLGNLIENALE-ALGPEPGGEISVTLHYRHGWLHCEVNDGDP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARASHGGDVVW 531
GI P+ +D +F SE G+GL L + + GG + V
Sbjct: 479 GIAPDKIDHIFDKGVSTKGSE-----RGVGLALVKQQVENLGGSIIV 520

>gi|37679787|ref|NP_934396.1| putative sensor kinase Cita [Vibrio vulnificus YJ016]
gi|37198532|dbj|BAC94367.1| putative sensor kinase Cita [Vibrio vulnificus YJ016]
Length = 539

Score = 150 bits (380), Expect = 5e-35

Identities = 147/533 (27%), Positives = 239/533 (44%), Gaps = 41/533 (7%)

Query: 17 IRFATRILVIQVAT--VALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIRBE 74
I F R+LVI + + L++ + G FA L Q + E AL + R +A++ + E
Sbjct: 6 ISFRKRMLVIMTSLGLIELLILVAAG-FAYLKYSQ-EQEMGQKALGVARFLATSTTVIEL 63

Query: 75 VALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV- 133
 + EL QA++ A F+V+ D GIRL HP +ERLG +
 Sbjct: 64 IENRDNVTYQOKFRELT---QALSAA-----FIVVGDREGIRLIHPVDERLGLPMR 111

Query: 134 -STSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMF 192
 + A GE ++ G+LG S R K +F V +G VSVG+ D + R+ F
 Sbjct: 112 GGDNARALEEGEAYISTARGSLGYSVRGKAAVFNSAGEV-IGVVS VG YLLDRLQDRIEPF 170

Query: 193 LAALALISVLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252
 L +++L + V+ R+++R LG +PEE+ L + I EGVL++
 Sbjct: 171 AWFLITMTLLVVAANALVSNYASRKPFQRAILGFEPEEIGRLYGELDVTMSTIKEGVLSID 230

Query: 253 PNGTIGVHNEQAQSMIGAGPMS--GRTLKEXXXXXXXXXXXXXXHGQ--HPETVAHNGRILY 308
 +G + N A ++G P + L + GQ H + N + L
 Sbjct: 231 SSGVLR SINRSAAQILGLDPAQVLNKP L S DALPASDLYRVLETGQEDHDI ELYLNQKRLI 290

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDI ELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
 + PV + +G V + R R +I EL+E+L + LR+Q HE N+++T +GL+
 Sbjct: 291 ANRSPVYVEGKIVGAVSSPRLRDEISELTEQLSQTKEYADLLRSQTHEHRNKINTISGLV 350

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXXXXXKGVSLRINS 426
 G + + +G + LI + + E G+ L +
 Sbjct: 351 QMGELDAVQQLIG---QETAHYQGLIEFLRDTIKDPLVAGMLLGKTERARELGLELVVEE 407

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDA--AVAGE-----APRWIELTMDADTLV 476
 + L +PED+ TILGNLI+NA DA A+A E + R IE+++ D ++
 Sbjct: 408 GARLEPLSAWLNPEEDITITILGNLIDNAFDATMSAIAQEGNFARSRRRTIEVSISDYGTEVI 467

Query: 477 ISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDV 529
 + V D G G+P+ F+T + ++ T G+GL L LA +GG +
 Sbjct: 468 LEVQDQGCGLPKQ---FSTEQLLEKGISSKATSTRGVGLYLVNQLAARYGGS 517

>gi|21223794|ref|NP_629573.1| putative two-component sensor kinase [Streptomyces c
 A3(2)]
 gi|6941977|emb|CAB72411.1| putative two-component sensor kinase [Streptomyces coe
 A3(2)]
 Length = 552

Score = 149 bits (376), Expect = 1e-34
 Identities = 150/543 (27%), Positives = 239/543 (44%), Gaps = 35/543 (6%)

Query: 19 FATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREVALD 78
 A ++ +Q +A+VV + Q + A A ++ ++A +P + E +
 Sbjct: 11 LAGQLFAMQAVLIAVVVVG YALFSYISDRGQAEZAAQRQARAVSLAIADSPSVAEAI RTP 70

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSF 138
 T +Q A T FV I + GIR +HP+ +G E
 Sbjct: 71 DPTAL-----LQPYAVRVMRDTDVDFVTIMNPEGIRWTHPEPT EIGHLFQGHIE 119

Query: 139 AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALAL 198
 A RG+ TGTLG S RA PI D VG VS G + + + R L AL+
 Sbjct: 120 RAQRGQTFETETYTGTLGPSVRAVTPIV--DDGRIVGLVSAGIKVEEISKRAQEQLTALS 177

Query: 199 ISVLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIG 258
 ++ +L+G + R R T G+ +EL + A + + EG+L L +
 Sbjct: 178 VAAGALLLGAVGTYVINARLRRHTHGMNADEL SRMHDYHQAALHAVREGLLM L DGQYRVA 237

Query: 259 VHNEQAQSMIGA-GPMSGRTLKEXXXXXXXXXXXXXXHGQHHPETVAHNG--RILYLD FHPVR 315

+ N+ + ++G G + G ++ + + H R+L ++ PV
Sbjct: 238 LINDGGRELLGVRGDIVGASVADLGLPSQLTGALLASEPRVDEVHLAAERVLVVNTSPVS 297
Query: 316 RGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDH 375
G++ G VVT+RD T++ L+ L+S R T ALR+Q HE ANR+HT LI+ GR +
Sbjct: 298 GGERR-GTVVTLRDVTEQLSLTGELNSERGFQALRSQAHEAANRLHTVVSLIELGRAEE 356
Query: 376 AAEF-LGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKEKGVSLRINSDTLILGTV 434
A EF ++ + ++ A ++E E+GV L ++ D+ + +
Sbjct: 357 AVSFATAELELAQALTDQVV--AAVSEFVLAALLLGKTAQANERGVELVVSQDSRLDDGL 414
Query: 435 KDP----EDVATILGNLINNAIDAAVAGEAPRWIELTLMDDA-----DTLVISVADSGPG 485
P D+ TILGNL++NA+DA G P + + +A LV+ V+D+G G
Sbjct: 415 LPPSLPARDLVTTILGNLVDNAVDAT-QGAVPSRVTVAAYTEASGAGGSELVLRVSDTGAG 473
Query: 486 I-PEGVDVFATATQIGDSEDNERETHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGV 544
+ P D+ Q G S G G+GL L R R HGG + V + GA F
Sbjct: 474 VDPHADL--VFQRGYSTKPAGEGGRGLGLALVRQAVRRHCGALTVTE-AEGCGARFEA 529
Query: 545 KLP 547
+LP
Sbjct: 530 RLP 532

>gi|2734636|gb|AAC28951.1| histidine kinase [Escherichia coli]
Length = 539

Score = 148 bits (374), Expect = 2e-34

Identities = 138/527 (26%), Positives = 232/527 (44%), Gaps = 43/527 (8%)

Query: 9 KNFKEVDIIRFATRILVIVQVATVALVVAICTGIFAVLMMDQMKEAHTALSIGRSVASN 68
K F + F RI ++ + V+A F D + A++ + +ASN
Sbjct: 8 KQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTASFEDYLT LHVRDMAMNQAKIIASN 67
Query: 69 PQIREEVALDTQTGANPSAEELADGDIQAVAQAANE---RTGALFVVTIDGLGIRLSHPD 125
+ V 'D + +A AN+ T +VVI D IRL HP+
Sbjct: 68 DSVISAVKTR-----DYKRLATIANKLQRTDFDYVVIGDRHSIRLYHPN 112
Query: 126 EERLGEQVSTSFEEAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDS 184
E++G + + + A+ +GE G++G + RAK PIF D V +G VS+G+
Sbjct: 113 PEKIGYPMQFTKQGALEKGESYFITGKSGMGMAMRAKTIPIFDDDGKV-IGVVSIGYLVSK 171
Query: 185 VYSRLPMFLAALA--LISVLGILIGVGVAMGMRWRVTLGLQPEELVTVQNQTAVID 242
+ S FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+
Sbjct: 172 IDSWRAEFLLPMAGVFVLLGILMLLSWFLAAHIR--RQMMGMEPKQIARVVRQQEALFS 229
Query: 243 GIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXHGHQHE 298
+ EG++A+ P+G I N A+ M+G G+ + E + +
Sbjct: 230 SVYEGLIAVDPHGYITAINRNARKMLGLSSPGRQWLKPIVEVVRPADFFTEQIDEKRQD 289
Query: 299 TVAH-NGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEF 357
VA+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE
Sbjct: 290 VVANFNGLSVIANREAIRSGDPLLGAIIISFRSKDEISTLNAQLTQIKQYVESLRTLREH 349
Query: 358 ANRIHTATGLIDAGRVDHAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXX 415
N + T GL+ ++ + L + LI S +
Sbjct: 350 LNWMTSLNGLL--QMKEYDRVLAMVQGESQAQQQLIDSLREAFADRQVAGLLFGKVQRA 406
Query: 416 XEKGVSLEI--NSDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDA 472

E G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+
Sbjct: 407 RELGLKMIIVPGSQLSQLPPLGLDSTEFAAIVGNLLDNAFEASLRSDGKNIKIVELFLSDEG 466

Query: 473 DTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKL 517
D +VI VAD G G+PE + +F E E HGIGL L

Sbjct: 467 DDVVIEVADQGCVPESLRDKIFEQGVSTRADEPGE----HGIGLYL 509

>gi|15612960|ref|NP_241263.1| two-component sensor histidine kinase [Bacillus halo
gi|25298482|pir|E83699 two-component sensor histidine kinase BH0397 (imported) -
halodurans (strain C-125)
gi|10173010|dbj|BAB04116.1| two-component sensor histidine kinase [Bacillus halod
Length = 532

Score = 147 bits (372), Expect = 4e-34

Identities = 147/544 (27%), Positives = 255/544 (46%), Gaps = 42/544 (7%)

Query: 21 TRILVIQVATVALVVAICTGI----FAVLMMDDQMKTEASHTALSIGRSVASNPQIREEVA 76
T++ ++ A V LVV + I +V +++++ E A++I R+VA + +
Sbjct: 6 TKLSILITALVCLVVIVALIITDLLVSVATSERLQSNIEEKATAISRTVA-----KAQWV 60

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTS 136
+D G EE +Q T LF+V+ D GIR SHP+ E +G++
Sbjct: 61 ID---GLENEEEER--VQTYTMEIQSATDVLFIIVMDMEGIRKSHPNPEEIGKRFVGG 114

Query: 137 FE-AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
E AA+ G E ++ TGTLG S RA PIF D +G V+VG V L + +
Sbjct: 115 DEVAALEGREHVSISTGTLGESLRAFTPIFN-DHGEQLGAVAVGISLQEVNDVLADNHTS 173

Query: 196 LALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ SV+GI++G+ A+ + +R LGL+P E+ +++ ++A++ E ++A+ G
Sbjct: 174 ILKGSVIGIIVGIIGALIVASYIKRALLGLEPFEIAKILEERSAMLQSAREAIIVDSKG 233

Query: 256 TIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXX-----HGQHPETVAHNGRILYL 309
TI + N+ A ++ MSG + + + E NG + +
Sbjct: 234 TITLVNKSALNLFKAGMSGDPGKVKVTEFMPTRSLEWVLKTRQPEFDEEQQMNGMTILV 293

Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ P+ D+ +G + T RD T+I + +++L V+ ALRAQ HEF N++H G++
Sbjct: 294 NRVPPIVNDDEVVGAISTFRDLTEIKQQAQQLTGKLYVEALRAQSHEFMNKLHVILGMVK 353

Query: 370 AGRVHDAAEFLGDI--SRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINS 427
+ +++ I R+ +H + + + EK ++L + +
Sbjct: 354 TESYDELNDXYIHQIVNHRSTELNHVI---KRIKDSVLGAFILGKLSYAREKHITLDVQTK 410

Query: 428 TLILGTVKDP--EDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPG 485
++I + ++ TILGNLI+NA++A + + + + L + L I V D+GPG
Sbjct: 411 SVIPKASSEQMVHELITILGNLIDNALEAVIKAKE-KTVLVQLEYSNERLHIRVQDTGPG 469

Query: 486 IPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCRALARSHGGDVWVIDRGTEGAVFG 543
IP+G D+F + G S E G GL L + GG + R T G F
Sbjct: 470 IPDGEQGDIF----KKGYSTKGE---NRGYGLYLKQSVKLGGAMEYESRAT--GMTFY 520

Query: 544 VKLP 547
V +P

Sbjct: 521 VDIP 524

>gi|30018746|ref|NP_830377.1| Two component system histidine kinase [Bacillus cere
gi|29894287|gb|AAP07578.1| Two component system histidine kinase [Bacillus cereus
Length = 535

Score = 147 bits (370), Expect = 7e-34
Identities = 130/527 (24%), Positives = 245/527 (46%), Gaps = 48/527 (9%)

Query: 41 IFAVLMMQMKTEAEHTALSIGRSVASNPQIREEEVALDTQTGANPSABELADGDIQAVAQ 100
+F ++ + ++ + AL + ++VA+ P+I+E + NP++ IQ +A+
Sbjct: 32 LFPYILSETVEEQIGKRALHVAKTVAAIPEIQEAFQKE-----NPAS-----IIQPIAE 80

Query: 101 AANERTGALFVVITDGLGIRLSHPDEERLGEQV--STSFZAAAMRGEETMAWETGTLGASA 158
T A F+V+ + GIR +HP+ +++GE++ + + G+ ++ TG+LG S
Sbjct: 81 KIRMDTEADFIVGNKEGIRYAHPERDKIGEXMVGGDNKGVLLLEGKSYVSKATGSLGPSL 140

Query: 159 RAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRW 218
R KVPI ++ + +G VSVGF ++ + ++ + I++G+LIGV ++ +
Sbjct: 141 RGKVPINQENEI-IGVSVGVGFSMADIHGAVEVYCKRVFWITIIGLLIGVIGSIYLAAS 199

Query: 219 ERVTGLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS---G 275
+R+ G++PER+ +L + + VI + EG++ + NG I + N+ A ++ G
Sbjct: 200 KRMMFGMEPEEBISSLYEEHSTVIQSVREGIIVIDKNGMISLVNQAAYDILSLDKQQNIIG 259

Query: 276 RTLKEXXXXXXXXXXXXXXHG--QHPETVAHNGRILYLDHFPVRRGDQDLGYVVTIRDRDI 333
+ G Q + G+ + + P++ ++ G V ++R ++++
Sbjct: 260 EFILNVIPNSTILDVLQTGEEQFDRQLNIKGQAVIANRLPIKVKNKVTGVVSSLRLKSEM 319

Query: 334 IELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFLGD---ISRNGGQ- 389
+L+ L + T ALRAQ HE+ N ++T +GLI DA E + + ++ Q
Sbjct: 320 DQLTAELSQTQYTEALRAQAHEYNLLYTLGSLIQLESYEDALELHKETAVYQDFVQF 379

Query: 390 -----SHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEG---VSLRINSDTLILGTVKDPEDVA 441
+P +G + E G +S I S+ V
Sbjct: 380 IMKRIQNPWLGGILIGFYNRARELKIDFMLDRESGLEKLSPHIESNY-----VV 428

Query: 442 TILGNLINNAIDAAVAGEA-PRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIG 500
+ILGNLI NA +A E + + + + D + ++I V DSG GI + +
Sbjct: 429 SILGNLITNAFEAIEKNEENDKKVRMFVTDIGEEILIEVEDSGQGIHDEIITSIFYKGFS 488

Query: 501 DSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKLP 547
E ER G GL + L G + I++G GA+F + LP
Sbjct: 489 TKEGGER----GYGLAKVKELVEDLNGSI-AIEKGDLCGALFIIALP 530

>gi|16764002|ref|NP_459617.1| sensory histidine kinase [Salmonella typhimurium LT2
gi|16419137|gb|AA119576.1| sensory histidine kinase in two-component regulatory s
DpiA [Salmonella typhimurium LT2]
Length = 553

Score = 145 bits (367), Expect = 2e-33
Identities = 145/547 (26%), Positives = 242/547 (44%), Gaps = 36/547 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMQMKTEAEHTALSIGRSVASNPQIREEEVA 76
+ F RI ++ + +VA + D + + A++ + +ASN I V
Sbjct: 16 LAFFLRIFLLILVVSFIVAALAAQYLSASFEDYLASHVRDMAMNQAKIIASNDSTIAAVK 75

Query: 77 LDTQTGANPSABELADGDIQAVAAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTS 136
N + LA +A T +VVI D IRL HP+ E++G + +
Sbjct: 76 -----NRDYKRLA-----IYANKLQRGTDFDYVVIGDRHSIRLYHPNPEKIGYPMQFT 123

Query: 137 FEAAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ RGE G++G + RAK PIP + +V +G VS+G+ + S FL
Sbjct: 124 KPGALERGESYFITGKGSIGMAMRAKTPIFDNEGNV-IGVVSIGYLVSKIDSWRLDFLLP 182

Query: 196 LALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+A + VL +++ + ++ R LG++P+++ +V+ Q A+ + EG++A+ P G
Sbjct: 183 MAGVFLVLLVLMMLLSWFFAAHRRQMLGMEPKQIARVVRQOEALFSSVYEGLIADVPEG 242

Query: 256 TIGVHNEQAQSMIGAGPMSGRT-----LKEXXXXXXXXXXXXXXGHPETVAH-NGRILYL 309
I N A+ M+G P GR + E + + +A+ NG +
Sbjct: 243 HITAINRNARKMLGL-PSPGRQWLGLIAEVVNPADFFTCQIAERRQDVMANFNGLSVIA 301

Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ +R G++ LG +++ R + +I L+ +L ++ +LR RHE N + T GL+
Sbjct: 302 NREAIRSGEELLGAIISFRSKDEIATLNAQLTQIKQYVESLRTLREHLNWMSTLNGLLQ 361

Query: 370 AGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNXXXXXXXXXXXXXXXXXGKVSRLI--N 425
E + S+ Q LI S + E G+ + I
Sbjct: 362 MKEYDRVREMVOGESQAQQQ---LIDSLRGAFADRQVAGLLFGKVQRARELGLKMVIVPG 418

Query: 426 SDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDADTLVISVADSGP 484
S L D + A I+GNL++NA +A++ E + IEL L D+ D +VI VAD G
Sbjct: 419 SQLHQLPEGLDSTEFAAIVGNLLDNAFEASLRTOEGDKTIELPLSDEGDEVVIEVADQGC 478

Query: 485 GIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEGAVF 542
G+PE + +F E E HGIGL L + GG V ++ G +F
Sbjct: 479 GVPEALREKIFEQGVSTRTEDEPGE---HGIGLYLIASVVGRCGG-VITLEDNDPCGTLF 533

Query: 543 GVKLPKV 549
+ LP V
Sbjct: 534 SLFLPKV 540

>gi|21219651|ref|NP_625430.1| putative two component system histidine kinase [Streptococcus
coelicolor A3(2)]
gi|10803161|emb|CAC13089.1| putative two component system histidine kinase [Streptococcus
coelicolor A3(2)]
Length = 548

Score = 145 bits (366), Expect = 2e-33
Identities = 157/511 (30%), Positives = 252/511 (49%), Gaps = 42/511 (8%)

Query: 63 RSVASNPQIREEVALDTQTGANP--SAEELADGDIQAVAQAANE---RTGALFVITDGL 117
R+ + + R AL Q A P ++ L +A+A N ++G V + D
Sbjct: 38 RATFNVRVEGRRTALAEQLAATPLVRSQLLRPVPQEBALAPLVNSTQTQSGVTSVTVADAH 97

Query: 118 GIRLSHPDEERLGEQVSTSFEAAMRGEETMAWETGTL----GASARAKVPIFAPDSSV-- 171
G +S D +G ++ + RG + +G L G A+V+P+
Sbjct: 98 GRIVSSTDPTLIGARLPRA-----RGAGVTSGWSGPLTVQGGRELVAQVPVLGATRQTLG 152

Query: 172 -PVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMG--MRRRWERTLGLQPE 228
+G V VG +V+ RL A+ L++ LG+ G+GVA + RR +R TLGL+P
Sbjct: 153 RHLGTVMVGEADPTVWQRLSG--ASSYLLAYLGVASGLGVAGSWLLARRVKRQTLGLEPR 210

Query: 229 ELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIG-AGPMSGRTLK----EXXX 283
E+ L +++ A++ GI EGV+AL P + + NE + ++ G++L +
Sbjct: 211 EIAGLABHREAMLYGIAEGVVALDPQHRLTLVNEMGRRLDLDPADCVGQSLDGLGIDGRL 270

Query: 284 XXXXXXXXXXXXHGQHP--ETVAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDIIELSERLD 341
P E V +GR+L ++ V + + LG V T+RDRT++ L +
Sbjct: 271 RDVLAGAAREAAEPRDEVVVRHGRVLMNRMVTVKDGRPLGSVTTLRDRTELARLEREIG 330

Query: 342 SVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNE 401
S R+ + LRAQ HEFAN++HT +GLI G + ++ +++ QS + S + +
Sbjct: 331 SFRSTSELLRAQAHEFANQLHTISGLIQIGEQBEVVRYVRGLNQR-RQSLDVTLSRRVRD 389

Query: 402 XXXXXXXXXXXXXXXXKEKGVSLRINSDTLILGTVK--DPEDVATILGNLINNAIDAABA-G 458
E+ V+LR+ SD L ++ D DVAT++GNL++NA+DAA A G
Sbjct: 390 TAVAALITAKSSSLAERRVALRV-SDRTALDRLEPADAADVATVVGNLVDNAVDAAAALG 448

Query: 459 EAPR-WIELTLMDDADTLVISVADSGPGI-PE-GVDVFATATQIGDSEDNERTHGHGIGL 515
+AP W+E+ L DA ++ I V DSGPG+ PE +VF+ + ER GIGL
Sbjct: 449 DAPEAWVEVELRQDAASVEIVVRDSDSGPGVAPELAREVFSHGFTTKAARQGER---GIGL 504

Query: 516 KLCRALARSHGGDVWVIDRGTEGDAVFGVKL 546
L R + HGG++ V + T +GAVF ++
Sbjct: 505 ALTRLVCERHGGGEISVTN--TPEGAVFTARM 533

>gi|23100706|ref|NP_694173.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
gi|22778940|dbj|BAC15207.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
Length = 528

Score = 144 bits (363), Expect = 5e-33
Identities = 141/543 (25%), Positives = 247/543 (45%), Gaps = 46/543 (8%)

Query: 22 RILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVALDTQT 81
+ LV+ V ++ + ++ DQ + AL+ +V+ P+++ +
Sbjct: 8 KFLVLGCILVTAIMLMVMVLYISYERDQTRQLIGQQALTIAVSEIPEVQHVI----- 61

Query: 82 GANPSAEELADGDI-QAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--STSFE 138
E D D+ Q + +++ A F+VI D +R +HPD +++G Q+ + +
Sbjct: 62 -----EHQKDADVLQPFIERIRKQSNAEFIVIGDRNSLRYTHPD PDKVGMQMVGGDNEQ 115

Query: 139 AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFEE---RDSVYSR-LPMFLA 194
A + GE ++ G+LGAS R K PIF D + +G VSVG+ DS++ + L FL
Sbjct: 116 ALVDGENYVSIANGSLGASVRGKSPIFNSDGD I-IGIVSVGYMISYVDSLQKQGLIGLFLV 174

Query: 195 ALALISVLGILIGVGVAMGMRWRERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
L+LI ++G+ +A +R+ T GL+P ++ + + + A+++ I EG++A
Sbjct: 175 WLSLIFIIGVAGSFLAKSIRKD---TFGLEPYQIARIYKERGALESIKEGLIATDQR 230

Query: 255 GTIGVHNEQAQSMIG-----AGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYL 309
G I + N A+ M+ G L G T+ N +L +
Sbjct: 231 GHITLVNYSKEMLHIRHDVIGKFPVQEVLPNTLAYVLTEEHREGSFETTI--NQTVLLV 288

Query: 310 DFHFPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ + G V + + R+D+ EL L V+ + LRAQ HE+ N+++ +G +
Sbjct: 289 RYKLIDDDGDYGGKVASFQVRSDDLQELIHTLSEVQQYSQDLRAQTHEYTNKLXVISGWLQ 348

Query: 370 AGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEKGVSLRINSDTL 429
G A +F+ + QS+ + +++ EK + IN +
Sbjct: 349 LGHTDKAKQFIHE-EVGKQOSYEKVLFEQISDSTIQAILIGKLSKASEKKIEFTINEGSH 407

Query: 430 ILGTVKDFE---DVATILGNLINNAIDAABAAGEAPRWIELTLMDDADTLVISVADSGPG 485

I + PE + TI+GN+I+NA DA V + P+ I++ L D + LVI VAD+G G
Sbjct: 408 I--NYQWPEQMTAQLVTIIGNIIDNAFVAVNTDNP-K-IDIFLTDMGNDLVIEVADNGTG 464
Query: 486 I-PEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVEGV 544
I P D + G S + + G+G+ L + AL G I +G VF V
Sbjct: 465 ISPADYD---NIMKQGYSTKDGQNRGYGLAL-VQAALLELQG--FLEITANEPNGTVFIV 518
Query: 545 KLP 547
+P
Sbjct: 519 YIP 521

>gi|16759585|ref|NP_455202.1| sensor kinase DpiB [Salmonella enterica subsp. enter
Typhi]
gi|29142642|ref|NP_805984.1| sensor kinase DpiB [Salmonella enterica subsp. enter
Typhi Ty2]
gi|25298491|pir|AP0579 sensor kinase DpiB (EC 2.7.3.-) [imported] - Salmonella e
subsp. enterica serovar Typhi (strain CT18)
gi|16501877|emb|CAD05102.1| sensor kinase DpiB [Salmonella enterica subsp. enteri
Typhi]
gi|29138273|gb|AA069844.1| sensor kinase DpiB [Salmonella enterica subsp. enteric
Typhi Ty2]
Length = 553

Score = 144 bits (362), Expect = 5e-33
Identities = 145/547 (26%), Positives = 241/547 (44%), Gaps = 36/547 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
+ F RI ++ + +VA + D + + A++ + +ASN I V
Sbjct: 16 LAFPLRIFLLILVSVFIVAALAAQYLSASFEDYLASHVRDMANQAKIIASNDIIAAVK 75
Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVIDGLGIRLSHPDEERLGEQVSTS 136
N + LA +A T +VVI D IRL HP+ E++G + +
Sbjct: 76 -----NRDYKRLA-----IIANKLQRGTDFFDYVVI GDRHSIRLYHPNPEKIGYPMQFT 123
Query: 137 FEAAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ RGE G++G + RAK PIF + +V +G VS+G+ + S FL
Sbjct: 124 KPGALERGESYFITGKSGSIGMAMRAKTPIFDNEGNV-IGVVSIGYLVSKIDSWRLDFFLLP 182
Query: 196 LALISVLGILIGVGVAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+A + VL +++ + ++ R LG++P+++ +V+ Q A+ + EG++A+ P G
Sbjct: 183 MAGVFVLLLVLMLLSWFFAAHRRQMLGMEPKQIARVVRQOEALFSSVYEGLIAVDPEG 242
Query: 256 TIGVHNEQAQSMIGAGPMSGRT----LKEXXXXXXXXXXXXXXXXXHGQHPETVAH-NGRILYL 309
I N A+ M+G P GR + E + + +A+ NG +
Sbjct: 243 HITAINRNARKMLGL-PSPGRQWLGLKIAEVVNPADFFTCQIAERRQDVMANFNGLSVIA 301
Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ +R G++ LG +++ R + +I L+ +L ++ +LR RHE N + T GL+
Sbjct: 302 NREAIRSGEELLGAIISFRSKDEIATLNAQLTQIKQYVESLRTL RHEHLNWMSTLNGLLQ 361
Query: 370 AGRVHDAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXXXXXKGVSLRI--N 425
E + S+ Q LI S + E G+ + I
Sbjct: 362 MKEYDRVREMVGESQAQQQ---LIDSLRGAFADRQVAGLLFGKVQRARELGLKMVIVPG 418
Query: 426 SDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDADTLVISVADSGP 484
S L D + A I+GNL++NA +A++ E IEL L D+ D +VI VAD G
Sbjct: 419 SQLHQLPEGLDSTEFAAIVGNLLDNAFEASLRTOEGDNTIELFLSDEGDEVVIEVADQGC 478

Query: 485 GIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCRALARSHGGDVWVIDRGTEDGAVF 542
G+PE + +F E E HGIGL L + GG V ++ G +F
Sbjct: 479 GVPEALREKIFEQGVSTRADEPGE---HGIGLYLIASYVGRCGG-VITLEDNDPCGTLF 533

Query: 543 GVKLPGV 549
+ LP V
Sbjct: 534 SLFLPKV 540

>gi|28898486|ref|NP_798091.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
gi|28806704|dbj|BAC59975.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
Length = 539

Score = 141 bits (355), Expect = 4e-32
Identities = 142/548 (25%), Positives = 244/548 (44%), Gaps = 36/548 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGI-FAVLMMDQMKTEAHTALSIGRSVASNPQIREEV 75
I F R+LVI + + + + F L ++Q + E AL + R +A + E+
Sbjct: 6 ISFRKRMLVIMTSLGLIELLLLVAAGFTYLVNQ-EHEMGEKALGVARFLAES-----EI 59

Query: 76 ALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVI TDGLGIRLSHPDEERLGEQVS- 134
++ P Q +A + GA F+VI D G+RL HP +ER+G+ +
Sbjct: 60 VIEMVEAQQPEP-----YQESFRALTKAIGAAFIVIGDNQGVRLIHPVDERIGKPMKG 112

Query: 135 -TSFEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFL 193
+ A + G+ ++ G+LG S R K IF ++ +G VSVG+ D + R+ FL
Sbjct: 113 GDNQRALVEGQSYVSTARGSLGYSVRGKAAIFDAQNI-IGVSVGYLLDRLQDRIEPL 171

Query: 194 AALALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSP 253
A L L+ V+ ++ V+ R+++R LG +PEE+ L + I EGV++
Sbjct: 172 AFLILMVVVVVANAVVSNYASRKFRAILGFEPPEEIGRLYGELEVTMTSTIKEGVLSIDA 231

Query: 254 NGTIGVHNEQAQSMIGA--GPMSGRTLKEXXXXXXXXXXXXXXHGQ--HPETVAHNGRILYL 309
G + N A ++G + L + GQ H + N + L
Sbjct: 232 QGVLRISINRSACQILGIDRDKALNKPLTDTLRSDLYTVLETGQEDHDIEIFLNHKRLIA 291

Query: 310 DFHPVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTALRAQRHEFANRIHTATGLID 369
+ P+ + +G V + R R +I EL+E+L + LR+Q HE N+++T +GL+
Sbjct: 292 NRSPIFVEGKIVGAVSSFRLRDEINELTEQLSQTKEYADLLRSQTHEHRNKLTISGLVQ 351

Query: 370 AGRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDDL 429
G + + +G + + Q+ + + E G+ L + +
Sbjct: 352 MGELEAVQKLIGQETAH-YQAMIEFLRDTIKDPLIAGMLLGKTERARELGLQLVVEGSR 410

Query: 430 I--LGTVKDPEDVATILGNLINNAIDAAVA-----GEAPRWIELTLMDDADTLVISV 479
+ L + ED+ TILGNLI+NA DA ++ R IE+++ D + +++ V
Sbjct: 411 LEPLTEWLNSDLVTILGNLIDNAFDATLSVIRDESNVASERRNIEVSVSDYGNEVILEV 470

Query: 480 ADSGPGIFEGVDVFATATQIGDSEDNERTHGHGIGLKLCRALARSHGGDVWVIDRGTEDG 539
+D G G+PE ++ T + G+GL L LA + G V ++ T G
Sbjct: 471 SDHGCGLPENIE---PQTLFKKGISTKSRQNRGVGLHLVNQLATRYHGHVEMLP-NTGHC 526

Query: 540 AVFGVKLP 547
V LP
Sbjct: 527 TRITVYLP 534

>gi|28211194|ref|NP_782138.1| sensor kinase dpiB [Clostridium tetani E88]

gi|28203634|gb|AA036075.1| sensor kinase dpiB [Clostridium tetani E88]
Length = 538

Score = 140 bits (352), Expect = 8e-32
Identities = 124/533 (23%), Positives = 251/533 (47%), Gaps = 52/533 (9%)

Query: 18 RFATRILVIQVATVALVVAICTGIFAVLMMQMK---TEAHTALSIGRSVASNPQIRE 73
+ RI V + LV+ I I L +M+ E AL + +++A +I+
Sbjct: 8 KITLRKIKVTLYVFILVMVI--SIIGYLSFKEMRELIEKERSKEALRLAQTAMTDEIKR 65

Query: 74 EVALDTQTGANPSAEELADGDIQAVAQAANERTGALEFVVITDGLGIRLSHPDEERLGEQV 133
+ + + LA +Q + +T F+V+ D G R SHP EE +G+ +
Sbjct: 66 NLN-----KKDSLA---LQYYVERVRLKTNVTFIVVIDMEGTRYSHPIEENIGKMI 113

Query: 134 STS--FEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSV---YS 187
E G+ ++ GTLG S R P++ + G VSVG + +V Y+
Sbjct: 114 KGGDHIEVINSQSQSYVSESVCTLGLSIRGFAPVYKDGEQI--GAVSVGILKGNVNLEVYN 171

Query: 188 RLPFMFLAALALISVLGILIGVGVAMGMRWRERVTLGLQPEELVTLVQNQTAVIDGIDEG 247
+L F+ * ++G++ G+ A + + GL+P+E+ L+ + A+++ +++G
Sbjct: 172 KLSKFIPFI----LVGLITGILGAYLLAHSIKNSIYGLEPKETALLSLKEAILESVEDG 227

Query: 248 VLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXX---HGQHP---ETV 300
++A+ +G I +N+ A++++G +S R L + + + P E
Sbjct: 228 IIAVDKSGNINLNYNKAENLLG---ISKRDLGKSVLNYPDESILEVLNTKKPLINVENK 284

Query: 301 AHNGRILYLDHFHPVRGDDQD-LGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFAN 359
+ G L +++ + D++ +G V+T D T I EL+E L V+ + +LRAQ HEF N
Sbjct: 285 INVGTTLMCNINILEDNRDKNFMGLVITFEDLTSIKELAEELTGVKKILWSLRAQNHEFMN 344

Query: 360 RIHTATGLIDAGRVHDAEFLGDIS-RNGGQSHPLIGSAHLNXXXXXXXXXXXXXKEK 418
++HT +GLI +++ +++ + GG S+ + + ++ E+
Sbjct: 345 KLHTISGLIQIEEYDMVVDYICELAYKRGGISYLI--NENIKIIPLOGLLLAKYNKCEEE 402

Query: 419 GVSLRINSDTLI--LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLV 476
+S I T + L + E++ +++GNL++N+++ AV + IE+ + ++ L
Sbjct: 403 KISFIKESTPLERLPNKMNSEEICSVVGNLVDNSME-AVEVDGTGKIEIEIRNNDKELF 461

Query: 477 ISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDV 529
+ V D+G GIP+ ++ +I E + + G+G+ + + + G++
Sbjct: 462 LMKVKGNGGIPKEIE-----EKIFLKEKSTKLGNRGLGMYIVKNIIEDKFGZI 509

>gi|23100675|ref|NP_694142.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
gi|22778909|dbj|BAC15176.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
Length = 533

Score = 136 bits (343), Expect = 9e-31
Identities = 135/543 (24%), Positives = 244/543 (44%), Gaps = 39/543 (7%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMM---DQMKTEAHTALSIGRSVASNPQIREEVA 76
TR+ ++ V LVV I +L+ +++K E A+ I R++A + +
Sbjct: 6 TRLSILITTLVCLVVIIVLITNDLLINYATGERLKENIEKAVIISRTMAKSEWV----- 60

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALEFVVITDGLGIRLSHPDEERLGEQVSTS 136
G EE IQ + T F+V+ D GIR SHP+ E +G+
Sbjct: 61 ---INGLQNKDEEKY---IQEYTNIEISRYTDLTFIVVMDMDGIRKSHPNPELIGKPFVGG 114

Query: 137 FEAAM--RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
 E + +G E ++ GTLG S RA PIF + +G VSVG + +
 Sbjct: 115 DEDTVLEQGIHISISEGTLGDSLRAFSPIFNEEGE-QIGAVSVGISLQEIDDVINNNHI 173

Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
 + + S++G++IG+ A + R +R+ GL+P ++ L++ ++A ++ EG++ + +
 Sbjct: 174 SNLISSIVGLIIGILGAWFIARYIKRILFGLPEPFIQAKLLKERSATLESAREGIITIDKD 233

Query: 255 GTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXXHGQHPETVAH--NGRILY 308
 I + N+ A + ++ G+ ++E Q V NG +
 Sbjct: 234 HKITIVNKAAMKVFEKAGITESPVGKNVEEVLPHSHLEDILKSKQPEMDVEQKINGVTIL 293

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
 + P+ D+ +G + T RD T++ +L+++L V+ ALRAQ HEF N++H G++
 Sbjct: 294 ANRMPIIVNDEVVGAISTFRDLTELKQLAKQLSGVKLYAEALRAQSHFEMNKLHVINGMV 353

Query: 369 DAGRVHDAAEFLGDI--SRNGCQSHPLIGSAHLNXXXXXXXXXXXXXXXXXKEGVSLRINS 426
 + +++ I RN +H + ++ + E+ V+L+I+
 Sbjct: 354 TTKSYDELDDYIKQIVNQRNDELNHVV--KNVKDSILAGFLLGKLSDARERDVNLQIDV 410

Query: 427 DTLILGTVKDP--EDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGP 484
 I + + + TI+GNL +NAID A+ + R I++ + D L I + D G
 Sbjct: 411 ABEIPASADNQVVHKLITIIGNLTDNAID-AIKSKENRTIDMYVSYKNDWLYIGIQDYGI 469

Query: 485 GIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARASHGGDVWVIDRGTEGAVFGV 544
 GI E + Q+ + + + G GL L R + GG + E G +F V
 Sbjct: 470 GIDEHIQ-----QQMFQKGYSTKGNNRGYGLYLVRSVETLGGSLRF--ETLEAGTIFEV 522

Query: 545 KLP 547
 ++P
 Sbjct: 523 EVP 525

>gi|15641613|ref|NP_231245.1| sensor kinase citA, putative [Vibrio cholerae O1 bio N16961]
 gi|11277516|pir|D82180 probable sensor kinase citA VC1605 [imported] - Vibrio ch (strain N16961 serogroup O1)
 gi|9656116|gb|AAF94759.1| sensor kinase citA, putative [Vibrio cholerae O1 biovar N16961]
 Length = 538

Score = 131 bits (329), Expect = 4e-29
 Identities = 138/541 (25%), Positives = 236/541 (43%), Gaps = 56/541 (10%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVA 76
 I F R+L+I + + + + + E AL + +A P + +
 Sbjct: 6 ITFRKRMLIIMTSLGLIELLLLVAAGFMYVKHSQEQQEVGQKALGVAFLAQTTPAVINMI- 64

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVTIDGLGIRLSHPDEERLGEQV--S 134
 +TG A D Q + + GA F+VI D GIRL HP +ER+G+ +
 Sbjct: 65 ---KTGR-----ASDDQQQSYRELTQLIGAAAFIVIGDNQGIRLVHPIDERIGKPMVGG 114

Query: 135 TSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
 + A + GE +++ G+LG S R K + + +G VSVG+ + + R+ FL
 Sbjct: 115 DNERALVEGEAYVSFAQGSGLKSVRGKAAVVDQHGQI-IGVVSVGYLIERLQDRVEPFLF 173

Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
 L ++L + V+ RR++R LG +PEE+ L + + EG++++

Sbjct: 174 YLIATALLVVGANALVSSYASRRFQRAILGFEPPEIARLYVELDVTMSTLKEGIISIDDK 233

Query: 255 GTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRI-----LYL 309
G + N+ A ++G L+ TV GR LYL

Sbjct: 234 GILRSINKSACEILG-----LRREQALNRRLTTILPESDLYTVLATGRTDHDIELYL 285

Query: 310 DFH-----FVRRGDQDLGYVVTIRDRTDI IELSERLDSVRTMTHALRAQRHEFANRIH 362
+ H P+ + +G V + R R +I EL+E+L R LR+Q HE N+++

Sbjct: 286 NKHWIIANRSPIVEGKVVGA VSSFRRLRDEINELTEQLAQTREYAEMLRSTHEHRNKLN 345

Query: 363 TATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEGVSL 422
T +GL+ G + + +G + H + L E E+ L

Sbjct: 346 TISGLLQMGELDAVQQQLIGQETE----HYQVLIEFLRETIKDPLIAGMLLGKTERAREL 400

Query: 423 RIN---SDTLILGTVK---DPEDVATILGNLINNAIDA---AVAGEAP-----RWIELTL 468
+ D L T+ EDV TILGNLI+NA +A A+ +P R IE+++

Sbjct: 401 GLELMVEDGARLETLP IHIKAEDVV TILGNLIDNAFEATLTARTLSPVPPERRVIEVSI 460

Query: 469 MDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGD 528
D + +++ V D G G+P+ ++ + T+ G S ++ G+GL L + LA + G

Sbjct: 461 SDFGNEIILEVDDQGCGLPKELEHWQL-TEKGS--SKAVQNRGVGLFLVKQLADRYQCQ 517

Query: 529 V 529
+

Sbjct: 518 L 518

>gi|23112843|ref|ZP 00098276.1| COG3290: Signal transduction histidine kinase regu
citrate/malate metabolism [Desulfitobacterium hafniense]
Length = 458

Score = 131 bits (329), Expect = 4e-29
Identities = 119/461 (25%), Positives = 217/461 (47%), Gaps = 18/461 (3%)

Query: 95 IQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEA-AMRGEETMAWETGT 153
IQ +A+ TG ++VI D IR SHP +R+G + E +++ +E ++ G

Sbjct: 2 IQPLAERIRLATGVEYIVIFDMEKIRYSHPYLDRIGTVFNDGDEELSLQRKEYLSQAVGV 61

Query: 154 LGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMLAALALISVLGILIGVGVAMG 213
+G S RA VP+ A + + VG V+VG ++ + L ++G+ +G +

Sbjct: 62 VGPSIRAFVPLADEGTRQVG VAVGILVPTIREIVGAIRVELYSSILIGLALGGLGSFY 121

Query: 214 MRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPM 273
+ ++ L+P ++ +++ + A+ +D+GV+AL I V NE+A + G

Sbjct: 122 LASNIKKNMFSLEBPSQIARMLSERVAIFQAMDDGVVALDMENRITVINEKACRIAGTSEK 181

Query: 274 S-GRTLKEXXXXXXXXXXXXXXH---GQHPETVAHNGRILYLD FHPVRRGDQDLGYVVTIRD 329
+ G L+E + E + +N +L +DF P+R +Q +G VVT+++

Sbjct: 182 AVGCPLQEFFAPTALSDFLETHDPAESTELILNNTWVL-VDELPIRVKEQVVG RVTLKE 240

Query: 330 RTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQ 389
+T++ +++E L V+T ALR Q HE N +HT GLI + A E++ ++ +

Sbjct: 241 KTSVRKMAEELTGKTFIEALRVQN HESLNTLHTIAGLIQLDKADQAMEYIYRVTEEQQE 300

Query: 390 SHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEGVSLRINSDTLI--LGTVKDPEDVATILGNL 447
+ S+ + E V + + D+ + L D + ILGNL

Sbjct: 301 VTKFL-SSKIMYPNVAGLLL GKYNRGKELKVDVLFDPDSRLSELPEGFDSNTLTIIILGNL 359

Query: 448 INNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNER 507

+ NA++A V + + + + L++SV D+GPGI A Q+ + +
Sbjct: 360 LENAMEAVVGSKISE-VHCRIKHEHHQLILSVEDTGPGIS-----LANQAQMYQWGFSTK 413

Query: 508 THGH-GIGLKLCLARSHGGDVWVIDRGTEGAVFGVKLP 547

+G+ GIGL L + GG + + + G FGV++P
Sbjct: 414 GNGNRGIGLSLVKQTVDLLGGTIEM--ETGKWGTRFGVRIP 452

>gi|18309513|ref|NP_561447.1| two-component sensor histidine kinase [Clostridium p
gi|18144190|dbj|BA980237.1| two-component sensor histidine kinase [Clostridium pe
13]
Length = 516

Score = 130 bits (326), Expect = 9e-29

Identities = 116/515 (22%), Positives = 230/515 (44%), Gaps = 43/515 (8%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
++F +IL+ + + +A+ +F + M + +T S++ P I+E++

Sbjct: 3 VKFENKILLWAILITFIPLALSFTLFIEDKLSYMDSDVRNTLKETAFSISEIPFIQEDL- 61

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--S 134

+ N +E I+A+ +V+ D G++ SH DE+++G+
Sbjct: 62 --SNGEINSRIQEYTKHFIEAINDVD-----IIVVADMRGVKYSHLDEKQIGQVFN 112

Query: 135 TSFRAAMRGEETMAWETGTGLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194

E +G + G++G + R P+ + VG + VG Y+ + + L
Sbjct: 113 DKKEVLTQSSSYSLMKGSMGETLRWFQPVMY--NGKQVGFIMVG---KYYNEIQL-LT 165

Query: 195 ALALISVLGI-----LIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVL 249

LI +G+ LI + ++ R+ ++ LG++PEE+ L + + +++ + EG++
Sbjct: 166 HKTLIKYMGFLFVLITILISKLFARKVKKAILGMEPEETIAALYKEKKIILNTVSEGII 225

Query: 250 ALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXGQHPETVAHNGRILYL 309

AL+ N I N+ +I G + LK+ + + G+ +++
Sbjct: 226 ALNKNNEITEINDNCYKLID-GFSKYKVLKLLPYIEENKPVEMKE---IILQKKVVFV 280

Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTALRAQRHEFANRIHTATGLID 369

P+ + + LG V+T+ DR DI +++ + V + LRA HEF N +H GLI
Sbjct: 281 TIQPIMKKG EYLGSVITLMDRNDIRKIAKEITGVDEVVKNLRANVHEFRNNLHVILGLIQ 340

Query: 370 AGRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXGKGVSLRINSDTL 429

G +A +++ + + + +++ + E+GV+ + ++
Sbjct: 341 LGEYEEARKYI--LKTQKIHENNSLKFSNVEDYYVRGLLSRELVAKERGVNFILTEESF 398

Query: 430 ILGTVK--DPEDVATILGNLINNAIDAAVAGEAP-RWIELTMDADATLVISVADSGPGI 486

+ G D D+ TILGNLI NA D+ V + +E+TL +D + + + V D+G I
Sbjct: 399 LFGNHNYVDSYDIVTILGNLIENAFDSCVCSSENKEVEVTLYEDDEKIEMQVRDNGKPI 458

Query: 487 PEGVD--VFATATQIGDSEDNERTHGHGIGLKLCL 519

+ +F ++G S E G G GL L +
Sbjct: 459 DNNIKERIF----ELGVSSKGE---GRGTGLSLVK 486

>gi|16077825|ref|NP_388639.1| two-component sensor histidine kinase [Bacillus subt
gi|21362406|sp|Q34427|CITS BACSU Sensor protein citS
gi|7428877|pir|E69600 two-component sensor histidine kinase citS - Bacillus subt
gi|2443240|dbj|BA22311.1| yf1R [Bacillus subtilis]
gi|2633082|emb|CAB12587.1| two-component sensor histidine kinase [Bacillus subtil

subtilis str. 168]
Length = 542

Score = 128 bits (321), Expect = 3e-28
Identities = 137/538 (25%), Positives = 240/538 (44%), Gaps = 35/538 (6%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMMDQMKTEAEHTALSIGRSVASNPQIREEVALDTQ 80
T+I+ + A + V+ + T AV + +AE A+ R+++ P ++E +
Sbjct: 12 TKIMGLIAALLVFIGVLTITLAVQHTQGERRQAEQLAVQTARTISYMPVVKELI----- 66

Query: 81 TGANPSAEELADG---DIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSF 137
E DG Q V + E+TGA + + + G S + L +++ S
Sbjct: 67 -----ERKDGHAQTQEVIEQMKEQTGAFAIYVLNEKGDIRSASGKSGL-KKLSRSR 117

Query: 138 EAAMRGEETMAWETGTLGASA-RAKVPIFAPDS--SVPVGEVSVGFERDSVYSRLPMFLA 194
E G ET G R PI S +G VSV F + + L
Sbjct: 118 EILFGGSHVS--ETKADGRRVIRGSAPIIKEQKGYSGVIGSVSVDFLOTETEQSIKKHLR 175

Query: 195 ALALISVLGILIGVGVAMGMRRRRWERVTGLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
L++I+VL +L+G A + + + TLGL+P E+ L + + A++ I EG++A +
Sbjct: 176 NLSVIAVLVLLLCFIGAAVLAKSIRKDTLGLLEPHEIAALYRERNAMLFAIREGIIATNRE 235

Query: 255 GTIGVHNEQAQSMIG-AGPMSGRTLKEXXXXXXXXXXXXXXGQH--PETVAHNCRILYLD 311
G + + N A M+ P+ + + G+ + V+ N ++ ++
Sbjct: 236 GVVTTMNVSAAEMLKLPEFVIHLPIDDVMPGAGLMSVLEKGEMLPNQEVSVNDQVFIINT 295

Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
+ +G Q G VV+ R++T++ +L + L VR + LRAQ HEF+N+++ GL++ G
Sbjct: 296 KVMNQGGQAYGIVVSFREKTELKKLIDTLTEVRKYSEDLRAQTHBFSNKLIALGLLELG 355

Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKGVSLRI--NSDTL 429
+A + + + + H L+ +++ EK V L I NS
Sbjct: 356 EYDEAIDLIKEYAIQNEQHDLLFH-NIHSQQVQAILLGKISKASEKKVKLVIDENSSLA 414

Query: 430 ILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGPIEG 489
L + TI+GNLI+NA + AVA ++ + + + D +VI V+D+GPG+P
Sbjct: 415 PLPAHIGLSHLITIIGNLIDNAFE-AVAEQSVKEVLFFITDMGHDIVIEVSDTGPQVPP- 472

Query: 490 VDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLP 547
+ + G S R G GL + R GG + + ++ T GAVF V +P
Sbjct: 473 -EKIEAVFERGYSSKGM---RGYGLANVKDSVRELGGWIELANQKT-GGAVFTVFIP 525

>gi|21398531|ref|NP_654516.1| HATPase_c, Histidine kinase-like ATPases [Bacillus a
gi|30260733|ref|NP_843110.1| sensory box histidine kinase [Bacillus anthracis str
gi|30254182|gb|AAP24596.1| sensory box histidine kinase [Bacillus anthracis str.
Length = 534

Score = 127 bits (318), Expect = 8e-28
Identities = 107/412 (25%), Positives = 191/412 (46%), Gaps = 31/412 (7%)

Query: 95 IQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSF EA-AMRGEETMAWETGT 153
IQ + TG F+V+ D GIR SHP+ +++G E A++G+E ++ GT
Sbjct: 75 IQTYTNRILKNTGVQFIVVMDMNGIRKSHPNPQKIGHHFIGGDEGPALKGKEHVSLAECT 134

Query: 154 LGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMG 213
LG S R VPIF+ ++ +G V+VG D+V R+ + + +G+L+G+ A+
Sbjct: 135 LGISM RVFVPIFS-ETGEQLGAVAVGISADNVKERVKESRHIIYIGVGVGLVGIIGAIL 193

Query: 214 MRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGP- 272
+ R ++ GL+P + +++ + ++ + EG++A+ + + N +A+ +
Sbjct: 194 LARHIKKSLEFGLPHRIAKILEERNTMLQSVKEGIIAVDKARVTLINNEAKRLFKKSGL 253

Query: 273 -----MSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVRRGDQD 320
M +KE + T+ N LY+ ++
Sbjct: 254 EEDFIGKDOVELYMPNSRIKEVLQTGEVQLNEEQNIYGITIVTNRVPLYVK-----EEI 306

Query: 321 LGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDHAAEFL 380
+G + T RD+T+I +L+E L +R ALRAQ HEF N++H GL + + ++
Sbjct: 307 VGAIATFRDKTEIRKLAELTGIRLYAEALRAQSHEFMNKMHVVLGLTHMKQYEELQKY- 365

Query: 381 GDISRNGGQSHPLIGSA--HLNEXXXXXXXXXXXXXXKEGVSLRINSDTLI--LGTVKD 436
IS + IG + EK + L I+ D+ + +
Sbjct: 366 --ISGMVSEHQYEIGGVMKRIKSPVFAGFLGKLSYAREKNIKLIISEDSYMPEIDDESI 423

Query: 437 PEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
++ TI+GNLI+NA++A E R +E+ + + D L I+V D+G GI E
Sbjct: 424 THELITIVGNLIDNALEAVTNCEKKR-VEVKIQHE-DILTITVQDTGKGIIQE 473

>gi|30018763|ref|NP_830394.1| Two-component sensor kinase yufl [Bacillus cereus AT
gi|29894304|gb|AAP07595.1| Two-component sensor kinase yufl [Bacillus cereus ATCC
Length = 534

Score = 125 bits (314), Expect = 2e-27
Identities = 107/412 (25%), Positives = 189/412 (45%), Gaps = 31/412 (7%)

Query: 95 IQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEA-AMRGEETMAWETGT 153
IQ + TG F+V+ D GIR SHP+ +++G E A++G+E ++ GT
Sbjct: 75 IQTYTNRILONTGVQFIVVMDMNGIRKSHPNPQKIGHHFIGGDEGPALKGKEHVSLAEGT 134

Query: 154 LGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMG 213
LG S R VPIF+ ++ +G V+VG D+V R+ + + +G+L+G+ A+
Sbjct: 135 LGISMRVFPVIFS-ETGEQLGAVAVGISADNVKERVKESRHHIYIGVGVGVVLVGIIGAIL 193

Query: 214 MRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGP- 272
+ R ++ GL+P + +++ + ++ + EG++A+ + + N +A+ +
Sbjct: 194 LARHIKKSLEFGLPHRIAKILEERNTMLQSVKEGIIAVDKARVTLINNEAKRLFKKSGL 253

Query: 273 -----MSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVRRGDQD 320
M +KE + T+ N LY+ +
Sbjct: 254 EEDFIGKDOVELYMPNSRIKEVLQTGEVQLNEEQNIYGITIVTNRVPLYVK-----GSI 306

Query: 321 LGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDHAAEFL 380
+G + T RD+T+I +L+E L +R ALRAQ HEF N++H GL + + ++
Sbjct: 307 VGAIATFRDKTEIRKLAELTGIRLYAEALRAQSHEFMNKMHVVLGLTHMKQYEELQKY- 365

Query: 381 GDISRNGGQSHPLIGSA--HLNEXXXXXXXXXXXXXXKEGVSLRINSDTLI--LGTVKD 436
IS + IG + EK + L I+ D+ + +
Sbjct: 366 --ISGMVSEHQYEIGGVMKRIKSPVFAGFLGKLSYAREKNIKLIISEDSYMPEIDDESI 423

Query: 437 PEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
++ TI+GNLI+NA++A E R +E+ + D L I+V D+G GI E
Sbjct: 424 THELITIVGNLIDNALEAVTNCEKKR-VEVKI-QHGDILTITVQDTGKGIIQE 473

>gi|23007702|ref|ZP_00049454.1| COG3290: Signal transduction histidine kinase regu

citrate/malate metabolism [Magnetospirillum
magnetotacticum]
Length = 279

Score = 124 bits (310), Expect = 6e-27
Identities = 95/279 (34%), Positives = 139/279 (49%), Gaps = 17/279 (6%)

Query: 110 FVVITDGLGIRLSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPFAPDS 169
+VV+TD G+R SHPD R+GE+VST + GE +TGTLG S R KVP+F P+
Sbjct: 1 YVVVITDDEGVRYSHPDPTTRIGERVSTDPVPLSGEVWTGTQTGTLGESWRVKVPVFGPEG 60

Query: 170 SVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRWRERVTGLQPEE 229
V VG SVG + L L L + +GV A + R R L+PEE
Sbjct: 61 DV-VGTASVGILESDLADDLADDLGWLLAALSVAALGVVCAAFVTRAVRRRIFRLEPEE 119

Query: 230 LVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIG--AGPMSGRTLKEXXXXXXX 287
+ L++ + A++ GI EGV+AL +G + + N++AQ ++G A GR +
Sbjct: 120 IGRLLLETRDAMLHGISEGVVALDRDGA VVLVNDEAQRLLGLIAAADAVGRPAHDVLDLPQLL 179

Query: 288 XXXXXHGQH-----PET----VAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDI 333
+ FE V R+L R + +G V+ +RD T++
Sbjct: 180 ALVPDTAETADDADAPAAGPEEGALVLAGERVLLARADRARDVGRVGTVLLLRDHTL 239

Query: 334 IELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGR 372
L LD R +T ALRAQ HEFAN++H +GL++ G+
Sbjct: 240 HALLRDLGARGLTDALRAQSHEFANKLHVVSGLLELGQ 278

>gi|16077512|ref|NP_388326.1| similar to two-component sensor histidine kinase [Yd
subtilis]
gi|15213974|sp|P96601|DCTS_BACSU Probable C4-dicarboxylate sensor kinase
gi|7428876|pir|A69771 two-component sensor histidine kinase homolog ydbF - Bacil
subtilis
gi|1881255|dbj|BAA19282.1| PROBABLE SENSORY TRANSDUCTION HISTIDINE KINASE. [Bacil
gi|2632745|emb|CAB12252.1| two-component sensor histidine kinase [Bacillus subtil
subtilis str. 168]
Length = 535

Score = 117 bits (293), Expect = 6e-25
Identities = 125/508 (24%), Positives = 214/508 (42%), Gaps = 37/508 (7%)

Query: 53 EAEHTALSIGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVW 112
E + ++ R+V+ +++E +A QT A A E +I+ + +A ++V
Sbjct: 42 BLKKRLMNTARTVSEMTEVKEALARKKQTEAVRHAVE-----BIRMINBAD-----YIV 90

Query: 113 ITDGLGIRLSHPDEERLGEQVSTSFEEAMRGEETMAWET-GTLGASARAKVPFAPDSSV 171
+ D IR +HP +G++ + E A E E G +G + RA P+ D +
Sbjct: 91 VMDMNHIRYTHPVSTSIGKKSEGADEEAFAEHIYFSEAKGEIGTAVRAFYPVKDQDLN- 149

Query: 172 PVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRWRERVTGLQPEELV 231
+G V VG + L +A I VL + G+ + + R ++ L+P E+V
Sbjct: 150 QIGVVLVGKTLPGIADILLHLKRDI AFIVLTLGFGLAGSFLARHIKKQMFQLEPHEIV 209

Query: 232 TLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGA-GPMSGRTLKEXXXXXXXXXXXXX 290
+ + +TA ++EGV+A+ I + NE+A+ + G + G+ + E
Sbjct: 210 RMYEERTATFHSMNEGVIAIDNRLVITIFNEKAKQIFEVQGD LIGKVIWEVLKDSRLPEI 269

Query: 291 XXHGQ--HPETVAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTH 348
+ + E + +G+++ P+ + +G V +DRT+ +++E L VR

Sbjct: 270 VERNKAVYNEEIRVSGKVIMSSRIPIVMKKKVIGAVAIFQDRTEAAKMABELTGVRNFVE 329

Query: 349 ALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXX 408
ALR Q HE N++HT GLI G+ A + S + + N+

Sbjct: 330 ALRVQNHEHMKLHTIAGLIQLGKSEKALQLAFQASTEQENVTEFLHRSIQND-AAAGLL 388

Query: 409 XXXXXXXXKEKGVSLRI--NSDTLILGTVKOPEDVATILGNLINNAIDA--AVAGEAPRWI 464
E G+++ I NS D D+ +LGNLI NA + V E R I

Sbjct: 389 LSKIRRGRELGIAPHIDENSSLQQFPFHVVDQHDIVVLLGNLIENAFGSFETVQSEDKR-I 447

Query: 465 ELTLMDDADTLVISVADSGPGI-----PEGVDVFATATQIGDSEDNERTHGHGIGLKLCR 519
++++ D L I + D+G GI P D T + G G G GL L +

Sbjct: 448 DISIEQTDDILAILIEDNGCGIEPTHTMPRLYDKGFTVNKTG-----GTGYGLYLVK 498

Query: 520 ALARSHGGDVWVIDRGTEDGAVFGVKLP 547
+ G + V D G F + P

Sbjct: 499 QIIDKSGGTIEV-DSHAGQGTSTFSIVFP 525

>gi|29375782|ref|NP_814936.1| sensory box histidine kinase [Enterococcus faecalis
gi|29343243|gb|AA081006.1| sensory box histidine kinase [Enterococcus faecalis v5
Length = 516

Score = 116 bits (291), Expect = 9e-25
Identities = 89/371 (23%), Positives = 174/371 (46%), Gaps = 33/371 (8%)

Query: 25 VIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVALDTQTGAN 84
VI +AT+ +++ G+ V + +++ E L++G +A P + E + D +

Sbjct: 13 VIFIATLIIMITFFYGVTTVQTIKEVRKNQEALLAVGEQLAIEPNVIEALKNDHYS--- 69

Query: 85 PSAEELADGDIQAVAQAANERTGAL---FVVITDGLGIRLSHPDEERLGEQVSTSFEA- 139
+EL +A R G + F+VI + GIRL+HPD +++G+ E

Sbjct: 70 ---DEL-----EAYTVRLGEIHQLDFIVIMNMQGIRLTHPDRQKIGKHFEFGGDEV 117

Query: 140 AMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSV--YSRLPMFLAAL 196
A++GEE ++ G+LG S R VP++ D +G V++G + S+ R

Sbjct: 118 ALKGEHLSVSQGSLSGESLRGFVPVY--DQKQIGVVAMGIKMTSLSQLIERTKNDYTVS 175

Query: 197 ALISV-LGILIGVGVAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
L+SV G ++ + V+ +++ L+P E+ L++ + A+++ + +L + +

Sbjct: 176 VLLSVGFGFILAIVVSYYLKKQLH---DLEPREIARLLEERNAMLEETKDAILVIDTDQ 231

Query: 256 TIGVHNEQAQSMIGAGPMSGRTL---KEXXXXXXXXXXXHGHQHPETVAHNIRILYLDHF 312
I + N +A M S L K H + + NG+ ++

Sbjct: 232 NILLANIEATKMYHNITNSEENLLGKKLSALVLSPEKLVVHSKTEQFYRQNGQDYFVSIA 291

Query: 313 PVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTALRAQRHEFANRIHTATGLIDAGR 372
P+ + +G+V+ +++ T+ ++E+L S T AL++Q HEF N++H GL+D

Sbjct: 292 PINVRKKTIGHVIFLKNATETFIVAEQLVSTTTYASALQSQSHEFMNKMHVIVGLVDLED 351

Query: 373 VHDAAEFLGDI 383
+L D+

Sbjct: 352 YEALKHYLADL 362

>gi|15615315|ref|NP_243618.1| two-component sensor histidine kinase [Bacillus halo
gi|15213978|sp|Q9K997|DCTS_BACMD Probable C4-dicarboxylate sensor kinase
gi|25298483|pir|H83993 two-component sensor histidine kinase BH2752 [imported] -

halodurans (strain C-125)

gi|10175373|dbj|BAB06471.1| two-component sensor histidine kinase [Bacillus halodurans]
Length = 532

Score = 115 bits (288), Expect = 2e-24
Identities = 114/450 (25%), Positives = 197/450 (43%), Gaps = 24/450 (5%)

Query: 110 FVVITDGLGIRLSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGA-SARAKVPIFAPD 168
++V+ + IR++HP ERL E E + T G + RA +PI
Sbjct: 91 YIVLLNMDRIRITHPIPERLQTPFVGGEDEPAPAEHIYLSKAKTEGVVTVRAFMPILNQ 150

Query: 169 SSVFVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMCMRRRWERTLGLQPE 228
VG VG S + F LI ++ L G + + +R T ++P+
Sbjct: 151 RE-QVGVAVVGSVLPSTYADMIQEFWQPALIGLITALEFGFWGSWLLASHIKRQTFNMEPD 209

Query: 229 ELVTLVQNQTAVIDGIDBGVLALSPNGTIGVHNEQAQSMIGAGPMS-GRTLKEXXXXXXX 287
EL L+ + A + I EGV+A++ + I + NE A+ M+G + GR + E
Sbjct: 210 ELAHLIVERDASFNAIHEGVVAINKHEKITIMNEAARRMLGVKEKAIGRNIHEVIPDTKL 269

Query: 288 XXXXXHGO--HPETVAHNGRILYLDHFVRRGDQDLGVVVTIRDRTDIELSERLDSVRT 345
G+ + GR+++ + P++ + +G + +D++D+ L+E L V+
Sbjct: 270 PEILSIGKPLYQREFYIQGRLVFSNRIPQIDGETVGAIAIFQDKSDVDRLAELTGVQA 329

Query: 346 MTHALRAQRHEFANRIHTATGLIDAGRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXX 405
ALR Q HE++N++HT GLI A +++ D+ + ++ ++
Sbjct: 330 FVDALRVQNHEYSNKLHTIAGLIQLDEGKKALQYIFDLEEEQEFGVGV-MQKIHNDSL 388

Query: 406 XXXXXXXXXXXXKEGVSLRINSDTLILGTVKDPEDVAT-----ILGNLINNAIDA-AVAGE 459
E GV + I D+ + PE V T I+GNLI+N++DA + +
Sbjct: 389 GLLLGKVSRLGKELGVQVIEKDESEF---IDHPEGVTTHDLVVIVGNLIDNSLDAFSSTQD 445

Query: 460 APRWIELTLMDDADTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKL 517
+ + + + ++ D L I V D+G GI E V +F + T G GIGL L
Sbjct: 446 QNKTVHVFIGEENDFLKIRVRDNGEGIREEVREKMFVRGFS-----TKSTSGRGIGLPL 499

Query: 518 CRALARSHGGDVWVIDRGTEGAVFGVKLP 547
+A+ G + V + G F + LP
Sbjct: 500 IQAIVERVEGKIEV-ESELNIGTTFSIYLP 528

>gi|21398509|ref|NP_654494.1| hypothetical protein predicted by GeneMark [Bacillus
A2012]
Length = 260

Score = 110 bits (276), Expect = 6e-23
Identities = 69/255 (27%), Positives = 143/255 (56%), Gaps = 14/255 (5%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAEHTALSIGRSVASNPQIREVA 76
++ RI + A + +V+ + + +F ++ + ++ + AL + ++VA+ P+I+E A
Sbjct: 6 LKLQPRITLTISALILVVLMLTSYLFYILSETVEEQIGKRALHVAKTVAAIPEIK--A 63

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--S 134
T+ NP++ IQ +A+ T A F+V+ + GIR +HP+ ++GE +
Sbjct: 64 FQTE---NPAS-----IIQPIAERIRMDTEADFIIVGNKEGIRYAHPERDKIGEAMIGG 114

Query: 135 TSFEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
+ + G+ ++ TG+LG S R KVPI ++ + +G VSVGF D ++ + ++
Sbjct: 115 DNKGVLLGKSYVSKATGSLGPSLRGKVPIRNOENI-IGVSVSGFSMDDIHGAVEVYVK 173

Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
+ I+++G+LIGV ++ + +R+ G++PEE+ +L + + VI + EG++ + N
Sbjct: 174 RVFWITIIGLLIGVIGSIYLAGSIKMMFMGMEPEEISSLYEEHSTVIQSVREGIIVIDQN 233
Query: 255 GTIGVHNEQAQSMIG 269
G I + N+ A ++
Sbjct: 234 GMISLVNQAAYDILA 248

>gi|28900618|ref|NP_800273.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
gi|28808998|dbj|BAC62106.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
Length = 524

Score = 110 bits (275), Expect = 7e-23
Identities = 104/435 (23%), Positives = 192/435 (44%), Gaps = 12/435 (2%)

Query: 98 VAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV-STSFEEAAMR-GEETMAWETGTLG 155
+ A + A F+ ++D GIRL+HP ER+G V E A+ GE +++ G+LG
Sbjct: 75 IINAVQAVSDADFITVSDRAGIRLAHPVAERVGLFVLGGDIERALENGESYLSYGVGSLG 134
Query: 156 ASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMR 215
S R PIF+ + V +G + VG+ D++ L L ++ + I + ++
Sbjct: 135 PSVRYISPIFSNEG DV-IGMIKVGYLIDTLDLWTSERLLPLISFGIIVAICTWLSWKFS 193
Query: 216 RRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSG 275
R L+P +L ++ V+ EG++A++ G++ + N+ A++M+ G
Sbjct: 194 RYVRTQMQUELEPWQLKQALKTHQGVLOATYEGVLVAINSEGSYLYLINDSARAMLNHYHQELG 253
Query: 276 RTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFVRRGD-QDLGYVVTIRDRTDII 334
+ + NG+ L ++ +R + G V ++RD+ ++
Sbjct: 254 NVFTDGIDNPESFSLKGDDYINGLIRVNGKNLVMNRVTLRTSTGEPYGAVFSLRDQNMH 313
Query: 335 ELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFLGDISRNGGQSHPLI 394
LSE++ V +R RHE+ N++ T +GL+ G +D A + QS
Sbjct: 314 VLSEKISQVTQYMNMRVARHEYQNKLTISGLLQMG-AYDKALSVCLSQAKASQSQLDS 372
Query: 395 GSAHLNEXXXXXXXXXXXXXXKEGVSLRIN--SDTLILGTVKDPEDVATILGNLNNAI 452
A + E GV+L I+ SD L E + ++GNL NA+
Sbjct: 373 LHALNSRPALSALILAKASKANELGVALSIDCQSDLSALSRRLSEEQLCGLIGNLAQNAL 432
Query: 453 DAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHG 512
+ AV G+ + + + A I V+++GP + DV ++G + + HG
Sbjct: 433 E-AVKGQENGHVHIGISESACEYTIQVSNNGPILLESEFDVLC---ELGFTTKQNKAD-HG 487
Query: 513 IGLKLCRALARSHGG 527
+G+ L R++ G
Sbjct: 488 VGMYLVR SIVEQNGG 502

>gi|29140597|ref|NP_803939.1| sensor kinase Cita [Salmonella enterica subsp. enter
Typhi Ty2]
gi|29136221|gb|AA067788.1| sensor kinase Cita [Salmonella enterica subsp. enteric
Typhi Ty2]
Length = 539

Score = 107 bits (268), Expect = 5e-22
Identities = 123/545 (22%), Positives = 238/545 (43%), Gaps = 33/545 (6%)

Query: 19 FATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVALD 78
F RI ++ + T +V+ T + +++ + AL +++ P++ E V
Sbjct: 15 FQNRIFLLILFTSTIVMLAITWYLTDTIKERLHYQVGQRALIQAMQISAMPELVEAV--- 71

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136
A +L+ I+A+ + A ++ + + G RL H + + +G+ + S
Sbjct: 72 -----EAHDLR--IKALIDPMRSFSDATYITVGNEKGQRLYHVNPD EIGKMEGGDS 122

Query: 137 FEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAAL 196
+A + ++ G+LG+S R K PI V +G VSVG+ + + S L + ++L
Sbjct: 123 DDALYNAKSYVSVRKGSLSGSSLRGKSPIQDSTGKV-IGIVSVGYTLEQLESWNLQISSL 181

Query: 197 ALISVLGILIGVGVAMGMRRRWERVTGLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256
+ +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +
Sbjct: 182 LFPMAILLVLLYCARRFSLHIKKQMLNMEPQQLSQLLIQQSVLFESVFEGLIAIDSHHR 241

Query: 257 IGVHNEQAQSMIG-AGPMS---GRTLKEXXXXXXXXXXXXXH-GQHPETVAHNGRILYLD 311
I N+ A+ ++ + P S G + + E V N +
Sbjct: 242 ITAINQTARLLNLSQPESELIGYAIHHIVLPEAFFXDAPQKNKKDEIVTFNQMKVIASR 301

Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
V +Q G+V++ R++ DI L+ +L VR LRA +HE N I T GL+
Sbjct: 302 MAVIIDNQPGQWVISFRNKDDINTLNLQLSQVRQYADNLRAVQHEHRNLSTIAGLLFLK 361

Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXSGVSLRINSDTLI- 430
R +A + S + + I S + + E G+ L + + +
Sbjct: 362 RYDNALALIQQSESHQKVLDPI-SHNFRDHHLAGLLIGKYRAKELGLELIFDPSSFVE 420

Query: 431 -LGTVKDPEDVATILGNLINNAIDAAGVAG-EAPRWIELTLMDDADTLVISVADSGPGIPE 488
L + + +I+GNL++NA +A + E R IE + + + ++I VAD G GI E
Sbjct: 421 HLPSSLSHNEWISIVGNLLDNAYNATLLNREGSRQIECLINSEGNEVIEVADQGCIDE 480

Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKL 546
+ +F ++ D HGIGL L + + GD+ ++D G +F + +
Sbjct: 481 NIRQHIFERGVTTHNNGD-----HGIGLWLVHSYVKQANGDI-IVDNNNSFGTIFTLYI 533

Query: 547 PGVME 551
P E
Sbjct: 534 PFTR 538

>gi|16759047|ref|NP_454664.1| sensor kinase cita [Salmonella enterica subsp. enter Typhi]
gi|25298488|pir|AH0508 sensor kinase cita (EC 2.7.3.-) [imported] - Salmonella e subsp. enterica serovar Typhi (strain CT18)
gi|16501337|emb|CAD01208.1| sensor kinase cita [Salmonella enterica subsp. enteri Typhi]
Length = 539

Score = 107 bits (267), Expect = 6e-22
Identities = 123/545 (22%), Positives = 238/545 (43%), Gaps = 33/545 (6%)

Query: 19 FATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVALD 78
F RI ++ + T +V+ T + +++ + AL +++ P++ E V
Sbjct: 15 FQNRIFLLILFTSTIVMLAITWYLTDTIKERLHYQVGQRALIQAMQISAMPELVEAV--- 71

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136
A +L+ I+A+ + A ++ + + G RL H + + +G+ + S
Sbjct: 72 -----EAHDLR--IKALIDPMRSFSDATYITVGNEKGQRLYHVNPD EIGKMEGGDS 122

Query: 137 FEAAMRGEETMAWETGTLGASARAKVPFAPDSSVPVGEVSVGFERDSVYSRLPMFLAAL 196
 +A + ++ G+LG+S R K PI V +G VSVG+ + + S L + +++L
 Sbjct: 123 DDALYNAKSYVSVRKGSLSGSSLRGKSPIQDSTGKV-IGIVSVGYTLEQLESWLNQLQISSL 181

Query: 197 ALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256
 + +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +
 Sbjct: 182 LFPMAILLVLLYCARRFSLHIKKQMLNMEPQQLSOLLIQSVLFESVFEGLIAIDSHHR 241

Query: 257 IGVHNEQAQSMIG-AGPMS---GRTLKEXXXXXXXXXXXXXH-GQHPETVAHNGRILYLDF 311
 I N+ A+ ++ + P S G + + E V N +
 Sbjct: 242 ITAINQTARLLNLSQPESELIGYAIHHIVLPEAFFYDAPQKNKKDEIVTFNQMKVIASR 301

Query: 312 HPVRRGDQDLGXVVTIRDRTDIIBLSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
 V +Q G+V++ R++ DI L+ +L VR LRA +HE N I T GL+
 Sbjct: 302 MAVIIDNQPGQWVISFRNKDDINTLNLQLSQVRQYADNLRAVQHEHRNLSTIAGLLFLK 361

Query: 372 RVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKEKGVSLRINSDTLI- 430
 R +A + S + + I S + + E G+ L + + +
 Sbjct: 362 RYDNALALIQQSES HQKVLDFI-SHNFRDHHLAGLLIGKYRAKELGLELIFDPSSSFE 420

Query: 431 -LGTVKDPEDVATILGNLINNAIDA AVAG-BAPRWIELTLMDDADTLVISVADSGPGIPE 488
 L + + +I+CNL++NA +A + E R IE + + + ++I VAD G GI E
 Sbjct: 421 HLPSSLSHNEWISIVGNLLDNAYNATLLNREGSRQIECLINSEGNEVIIIEVADQCGGIDE 480

Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARALSHGGDVWVIDRGTEDGAVFGVKL 546
 + +F ++ D HGIGL L + + GD+ ++D G +F + +
 Sbjct: 481 NIRQHIFERGVTTHNNGD-----HGIGLWLVSYSYVKQANGDI-IVDNNNSFGTIFTLYI 533

Query: 547 PGVME 551
 P E
 Sbjct: 534 PFTRZ 538

>gi|1705888|sp|P52687|CITA_KLEPN Sensor kinase cita
 gi|2126138|pir||S70538 signal-transducing histidine kinase cita - Klebsiella pneu
 gi|924991|gb|AAC44733.1| sensor kinase Cita
 Length = 547

Score = 106 bits (265), Expect = 1e-21
 Identities = 120/541 (22%), Positives = 236/541 (43%), Gaps = 33/541 (6%)

Query: 19 PATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVALD 78
 F RI ++ + T +V+ + + + + AL +++ P++ E V
 Sbjct: 20 FQNRIFLLILFTSTIVMLAMSWYLTIDITEERLHYQVGQRALIQAMQISAMPELVEAV--- 76

Query: 79 TQTGANPSAEELADGDIOAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136
 +LA I+A+ + A ++ + D G RL H + + +G+ + S
 Sbjct: 77 -----QKRDAR--IKALIDPMRSFSDATYITVGDAQGRLYHVPDEIGKSMEGGDS 127

Query: 137 FEAAMRGEETMAWETGTLGASARAKVPFAPDSSVPVGEVSVGFERDSVYSRLPMFLAAL 196
 EA + + ++ G+LG+S R K PI V +G VSVG+ + + + L + +++L
 Sbjct: 128 DEALINAKSYVSVRKGSLSGSSLRGKSPIQDATGKV-IGIVSVGYTIEQLENWLSLQISSL 186

Query: 197 ALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256
 + + +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +
 Sbjct: 187 LIPMAIMLLLLLFCARRFSLHIKKQMLNMEPQQLSOLLIQSVLFESVFEGLIAIDSDYK 246

Query: 257 IGVHNEQAQSMIGAG----PMSGRTLKEXXXXXXXXXXXXXH-GQHPETVAHNGRILYLDF 311

I N+ A+ ++ + G+ + + E V N +
 Sbjct: 247 ITAINQTARRLLNLSQPEPTLIGKRISVISQEVFFYDAPQTNKKDEIVTFNQIKVIASR 306
 Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
 V ++ G+V++ R + DI LS +L V+ LRA +HE N I T GL+
 Sbjct: 307 MAVILNNEPQGWVISFRSKDDINTLSLQLSQVQYADNLRAVQHEHRNLISTIAGLLFLK 366
 Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEGVSLRINSDTLI- 430
 R + A E + S + + I + + + E G+ L + + +
 Sbjct: 367 RYNQALELIQQQSESHQKVIDFI-ARNFQDNHLAGLLIGKYYRAKELGLELIFDPACFVD 425
 Query: 431 -LGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
 L T + +I+GNL++NA +A++ + + IE + D ++I +AD G GI E
 Sbjct: 426 RLPTALSHNEWISIVGNLLDNAYNASLRQPQGSQIECLINSQGQEVIIIEIADQCGGIDE 485
 Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKL 546
 + +F S+D HGIGL L R+ GG + V++ G +F + +
 Sbjct: 486 ALRDRIFERGVTSSASKD-----HGIGLWLVRSYVEQAGGSI-VVENNIPFGTIFTLYI 538
 Query: 547 P 547
 P
 Sbjct: 539 P 539

>gi|27366560|ref|NP_762087.1| Signal transduction histidine kinase regulating citr
 metabolism [Vibrio vulnificus CMCP6]
 gi|27358126|gb|AA007077.1| Signal transduction histidine kinase regulating citrat
 metabolism [Vibrio vulnificus CMCP6]
 Length = 519

Score = 104 bits (260), Expect = 4e-21
 Identities = 99/428 (23%), Positives = 194/428 (45%), Gaps = 15/428 (3%)

Query: 106 TGALFVVITDGLGIRLSHPDEERLG-EQVSTSFEEAAMR-GEETMAWETGTLGASARAKVP 163
 + A F+ ++D GIRL+HP ER+G V + A+ GE ++ G+LG S R P
 Sbjct: 80 SDADFITVSDEEGIRLAHPVSEVRGLPVVGGDIQRALNLGEAYLSQSVGSLGPSVRYISP 139
 Query: 164 IFAPDSSVPVGEVSVGF--ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERV 221
 IF+P+ V VG V VG+ E +++SR + L L +V + + + ++ ++
 Sbjct: 140 IFSPEGEV-VGMVKVGYLVETLNLWSREKLL--PLLLFAVSALSFLLLSWRFSSYVKKQ 196
 Query: 222 TLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEX 281
 L+P +L ++ V+D E V+A++ G I + N+ A++++ + G+ K+
 Sbjct: 197 MQDLEPWQLKQALKTHQGVLDATHEAVAVNQGNIIYLANDAARAILRQSELVGKETKQL 256
 Query: 282 XXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVRGD-QDLGYVVTIRDRTDIIELSERL 340
 + + ++ +R + + G V T+R R+++ LS+R+
 Sbjct: 257 DDASHLFHLDGDDFLDKVAQLGSDGVIINRVMTRTSNGEAGAVFTLRORSELQALSDRI 316
 Query: 341 DSVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAEF-LGDISRNGGQSHPLIGSAHL 399
 V ++R HE N++ +GL+ G A L ++N + L G +
 Sbjct: 317 SQVDKYLESMRVTHHEHQNKLSVISGLLQMGAFDKALSVCLAQAQONQTRIDSLQGVKSM 376
 Query: 400 NEXXXXXXXXXXXXXXXXXXKEGVSLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGE 459
 + + +++ D L E V +++GNLI+N ++A G+
 Sbjct: 377 PQLTALLAKLSKARESNQSLNIACYGDLGSLTQRVSEQVCSLVGNLIDNGLEAC-QGQ 435
 Query: 460 APRWIELTLMDDADTLVISVADSGPGIPEGVDFATATQIGDSEDNERTHGHGIGLKLCL 519
 + + L + + +++ +GP + E ++ S E HGIGL L +

Sbjct: 436 NDA TMVVKLRETEEEFILTFSSNNGPSLDEEDLES LCRWGYSTKSATGE---HGIGLHLVK 491

Query: 520 A-LARSHG 526

+ L+ +HG

Sbjct: 492 SILSRAHG 499

>gi|16763443|ref|NP_459058.1| putative transcriptional regulator [Salmonella typhi]
gi|16418548|gb|AA19017.1| putative transcription regulator [Salmonella typhimuri]
Length = 539

Score = 103 bits (256), Expect = 1e-20

Identities = 125/545 (22%), Positives = 238/545 (43%), Gaps = 33/545 (6%)

Query: 19 FATRILVIOVATVALVVAICTGIFAVLMDQMKTAEHTALSIGRSVASNPQIREEVALD 78

F RI ++ + T +V+ T + +++ + AL +++ P++ E V

Sbjct: 15 FQNRIFLLILEFTSTIVMLAITWYLTDPITKERLHYQVGQRALIQAMQISAMPELVEAV--- 71

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136

A +L+ I+A+ + A ++ + + G RL H + + +G+ + S

Sbjct: 72 -----EAHDLR--IKALIDPMRSFSDATYITVGNEKGQRLYHVNPFDEIGKYMEGCDS 122

Query: 137 FEAMARGEETMAWETGTLGASARAKVIPAPDSSVFGVSVGFERDSVYSRLPMFLAAL 196

+A + ++ G+LG+S R K PI V +G VSVG+ + + S L + +++L

Sbjct: 123 DDALYNKASYVSVRKGS LGSSLRGKSPIQDSTGKV-IGIVSVGYTTLEQLESWNLQISSL 181

Query: 197 ALISVLGILIGVGVMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256

L +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +

Sbjct: 182 LFPMALLLLVLVLYCARRFSLHIKKQMLNMFQQLSQLLIQQSVLPFESVFEGLIAIDSHHR 241

Query: 257 IGVHNEQAQSMIG-AGPMS---GRTLKEXXXXXXXXXXXXXX-H-GQHPETVAHNGRILYLD 311

I N+ A+ ++ + P S G + + E V N +

Sbjct: 242 ITAINQTARRLLNLSQPESELIGYAIHHVVLPEAFFYDAPQKNKKDEIVTFNQMKVIASR 301

Query: 312 HPVRRGDQDLGYVVTIRDRDTIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371

V +Q G+V++ R++ DI LS +L VR LRA +HE N I T GL+

Sbjct: 302 MAVIIDNQPGQWVISFRNKDDINTLSLQLSQVROYADNLRVQHEHRNLISTIAGLLFLK 361

Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXEGVSLRINSDTLI- 430

R +A + S + + I S + + E G+ L + + +

Sbjct: 362 RYDNALALIQQQSESHQKVLDFI-SHNRFDHHLAGLLIGKYRAKELGLELIFDPSSFVE 420

Query: 431 -LGTVKDPEDVATILGNLINNAIDAAG- EAPRWIELTLMDDADTLVISVADSGPGIPE 488

L + + +I+GNL++NA +A + E R IE + + + +I VAD G GI E

Sbjct: 421 HLPSSSLSHNEWISIVGNLLDNAYNATLLNREGSRQIECLINSEGNEVIIEVADQCGIDE 480

Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKL 546

+ +F ++ D HGIGL L + + GD+ ++D G +F + +

Sbjct: 481 NIRQHIFERGVTTTHNNGD-----HGIGLWLVSIVKQANGDI-IVDNNNPFGTIIFTLYI 533

Query: 547 PGVME 551

P E

Sbjct: 534 PFTRE 538

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF
Posted date: Jan 14, 2004 12:40 AM
Number of letters in database: 528,039,549
Number of sequences in database: 1,605,642

Lambda	K	H
0.317	0.135	0.386

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 51,380,962
Number of Sequences: 1605642
Number of extensions: 2020487
Number of successful extensions: 5969
Number of sequences better than 10.0: 273
Number of HSP's better than 10.0 without gapping: 20
Number of HSP's successfully gapped in prelim test: 253
Number of HSP's that attempted gapping in prelim test: 5749
Number of HSP's gapped (non-prelim): 305
length of query: 551
length of database: 528,039,549
effective HSP length: 130
effective length of query: 421
effective length of database: 319,306,089
effective search space: 134427863469
effective search space used: 134427863469
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 76 (33.9 bits)